

STIC-Biotech/ChemLib

167633

From: Foley, Shanon
Sent: Tuesday, October 04, 2005 9:03 AM
To: STIC-Biotech/ChemLib
Subject: Database Search Request

Requester:
Shanon Foley (TC1600)
Art Unit:
1648
Employee Number:
77851
Office Location:
3C21
Phone Number:
2-0898
Mailbox Number:

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Case serial number:
10/694247
Class / Subclass(es):

Earliest Priority Filing Date:

Format preferred for results:
Paper

Search Topic Information:

Please search amino acid SEQ ID NO: 2. I am interested in anything that has at least 70% sequence identity with this sequence. Please expand hit list as appropriate so that all relevant answers are listed. If the list is unusually, large, please put the results on a disc.

Thank you.
Special Instructions and Other Comments:

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 10/5
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
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WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: October 5, 2005, 10:03:10 ; Search time 166 Seconds
(without alignments)
400.740 Million cell updates/sec

Title: US-10-694-247-2

Perfect score: 907
Sequence: 1 CYSRKLMDARENLKILDR.....TVSTTLQKRLTKGGDLNSP 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1500 summaries

Database : A_GeneSeq_16Dec04:*

- 1: geneSeqp19808:*
- 2: geneSeqp19908:*
- 3: geneSeqp20008:*
- 4: geneSeqp20018:*
- 5: geneSeqp20028:*
- 6: geneSeqp20038:*
- 7: geneSeqp20048:*
- 8: geneSeqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	907	100.0	172 2 AAR54768	AAR54768 Sheep int
2	907	100.0	172 2 AAR9397	AAR9397 Ovine tau
3	907	100.0	172 2 AAW31698	AAW31698 Mature ov
4	907	100.0	172 2 AAW44110	AAW44110 Mature ov
5	907	100.0	172 5 ABB07588	ABB07588 Ovine int
6	907	100.0	172 7 ADI17857	ADI17857 Mature int
7	907	100.0	172 8 ADM79177	ADM79177 Mature ov
8	907	100.0	172 8 ADS13613	ADS13613 Sheep int
9	907	100.0	172 2 AAR04540	AAR04540 Ovine tro
10	905	99.8	172 2 AAR09294	AAR09294 Ovine tro
11	905	99.8	172 8 ADM79195	ADM79195 Interfero
12	904	99.7	195 2 AAR24942	AAR24942 Sequence
13	900	99.2	172 4 AAB31457	AAB31457 Amnio aci
14	900	99.2	172 5 AAO21461	AAO21461 Ovine int
15	899	99.1	172 5 ABB07589	ABB07589 Recombina
16	899	99.1	172 8 ADM79178	ADM79178 Mature ov
17	899	99.1	172 4 ADS13614	ADS13614 Recombina
18	898	99.0	172 4 AAB31462	AAB31462 An ovine
19	897	98.9	195 2 AAR24941	AAR24941 Sequence
20	897	98.9	195 2 AAR24945	AAR24945 Sequence
21	896	98.8	172 4 AAB31468	AAB31468 An ovine
22	896	98.8	172 4 AAB31466	AAB31466 An ovine
23	896	98.8	172 4 AAB31464	AAB31464 An ovine
24	895	98.7	172 4 AAB31459	AAB31459 An ovine
25	894	98.6	172 4 AAB31467	AAB31467 An ovine

26	894	98.6	172 4 AAB31465	AAB31465 An ovine
27	894	98.6	172 4 AAB31460	AAB31460 An ovine
28	892	98.3	195 2 AAR24944	AAR24944 Sequence
29	892	98.3	172 4 AAB31461	AAB31461 An ovine
30	890	98.1	172 4 AAB31463	AAB31463 An ovine
31	883	97.4	195 1 AAP91396	AAP91396 Isoform o
32	874	96.4	195 2 AAR24943	AAR24943 Sequence
33	857.5	94.5	196 4 AAB49784	AAB49784 Ovi TP-1
34	857.5	94.5	196 7 ADF94976	ADF94976 Sheep IFN
35	786	86.7	152 8 ADS16363	ADS16363 Human int
36	723	79.7	195 4 AAB49783	AAB49783 Bovine TP
37	723	79.7	195 5 ABB08641	ABB08641 Bovine int
38	723	79.7	195 5 ADF94975	ADF94975 Bovine IF
39	720	79.4	195 2 AAR04539	AAR04539 CDNA clon
40	691	76.2	173 2 AAW70809	AAW70809 A tau mod
41	649	71.6	171 7 ADG42697	ADG42697 Human int
42	649	71.6	171 7 ADJ55766	ADJ55766 Peptide h
43	649	71.6	171 8 ADM76604	ADM76604 Human NOV
44	647	71.3	173 2 AAW70808	AAW70808 A tau mod
45	632	69.7	173 2 AAW56435	AAW56435 Amnio aci
46	628	69.2	173 2 AAW70814	AAW70814 A human i
47	628	69.2	173 2 AAW56433	AAW56433 Amnio aci
48	628	69.2	173 2 AAW70812	AAW70812 A human i
49	627	69.1	173 2 AAW56434	AAW56434 Amnio aci
50	627	69.1	173 2 AAW70813	AAW70813 A human i
51	621	68.5	173 2 AAW56437	AAW56437 Amnio aci
52	615	67.8	173 2 AAW56440	AAW56440 Amnio aci
53	614	67.7	173 2 AAW56439	AAW56439 Amnio aci
54	612	67.5	172 2 AAW09278	AAW09278 Human mat
55	612	67.5	172 2 AAR99398	AAR99398 Human tau
56	612	67.5	172 2 AAW31699	AAW31699 Human int
57	612	67.5	172 2 AAW44111	AAW44111 Synthetic
58	612	67.5	172 2 AAW44117	AAW44117 Mature hu
59	612	67.5	173 2 AAW70811	AAW70811 A human i
60	612	67.5	195 2 AAW09288	AAW09288 Human com
61	612	67.5	195 2 AAW44106	AAW44106 Human int
62	611	67.4	173 2 AAW74460	AAW74460 Human int
63	609	67.1	172 2 AAR54769	AAR54769 Human int
64	609	67.1	172 2 AAW09277	AAW09277 Human mat
65	609	67.1	172 4 AAB49169	AAB49169 Human int
66	609	67.1	173 2 AAW56438	AAW56438 Amnio aci
67	609	67.1	173 2 AAW56436	AAW56436 Amnio aci
68	609	67.1	173 2 AAW70810	AAW70810 Amnio aci
69	609	67.1	195 2 AAR54770	AAR54770 Human int
70	604	66.6	171 2 AAW09279	AAW09279 Human mat
71	604	66.6	171 2 AAW44116	AAW44116 Human int
72	600.5	66.2	194 4 AAB49777	AAB49777 Human pla
73	600.5	66.2	194 7 ADF94969	ADF94969 Human pla
74	599	66.0	172 2 AAW09281	AAW09281 Human mat
75	599	66.0	172 2 AAR93939	AAR93939 Human tau
76	599	66.0	172 2 AAW31700	AAW31700 Human int
77	599	66.0	172 2 AAW44108	AAW44108 Mature hu
78	599	66.0	173 2 AAW74461	AAW74461 Human int
79	599	66.0	195 2 AAW09289	AAW09289 Human com
80	599	66.0	195 2 AAW44107	AAW44107 Human int
81	596	65.7	172 2 AAW09280	AAW09280 Human mat
82	582	64.2	195 1 AAP30076	AAP30076 Sequence
83	582	64.2	195 2 AAW73227	AAW73227 Bovine in
84	582	64.2	195 2 AAW83898	AAW83898 Bovine in
85	582	64.2	195 5 ABG32983	ABG32983 Bovine le
86	576	63.5	195 2 AAR04541	AAR04541 Bovine in
87	525	57.9	172 2 AAW09276	AAW09276 Human mat
88	521	57.4	166 8 ADM79185	ADM79185 Interfero
89	518	57.1	166 8 AAY05806	AAY05806 Human int
90	510	56.2	166 8 ADM79188	ADM79188 Interfero
91	510	56.2	166 8 ADM79186	ADM79186 Interfero
92	502	55.3	166 2 AAY05810	AAY05810 Human int
93	502	55.3	166 8 ADM79192	ADM79192 Interfero
94	498	54.9	166 2 AAY05811	AAY05811 Human int
95	498	54.9	166 8 ADM79193	ADM79193 Interfero
96	489	53.9	195 1 AAP60403	AAP60403 Equine IF
97	484	53.4	166 2 AAY05809	AAY05809 Human int
98	484	53.4	166 8 ADM79191	ADM79191 Interfero

99	481	53.0	172	6	ABP96600	Hybrid	int	172	438	48.3	166	8	AD129652	Ad129652	Human	int
100	479	52.8	166	2	AAy05812	Human	int	173	438	48.3	166	8	AD129623	Ad129623	Human	int
101	479	52.8	166	8	AdM79194	Interfero		174	438	48.3	166	8	AD129620	Ad129620	Human	int
102	473	52.1	172	4	ABa49170	Human	int	175	438	48.3	166	8	AD129647	Ad129647	Human	int
103	473	52.1	173	1	AAp70330	Sequence		176	438	48.3	166	8	AD129667	Ad129667	Human	int
104	473	52.1	195	1	AAp60253	Interfero		177	438	48.3	166	8	AD188857	Ad188857	Human	cyt
105	473	52.1	195	2	AAp66198	E.coli ST		178	438	48.3	166	8	AD032386	Ad032386	Human	int
106	473	52.1	195	2	AAy22635	Human	int	179	438	48.3	167	2	AAr11531	AAr11531	Consensus	
107	473	52.1	195	3	AAr13433	Human	int	180	438	48.3	167	8	AD087759	Ad087759	rs1FN-co.	
108	473	52.1	195	5	ABb07439	Interfero		181	438	48.3	167	8	ADr97080	Adr97080	Consensus	
109	473	52.1	195	5	AdM13727	Human	int	182	438	48.3	167	8	ADr87295	Adr87295	Consensus	
110	473	52.1	195	8	ADN10817	Human	int	183	438	48.3	189	5	AAg78567	AAg78567	Human	int
111	473	52.1	195	8	ADN49747	Human	int	184	438	48.3	189	6	AAE14832	AAE14832	Human	int
112	473	52.1	195	8	ADs16327	Human	int	185	438	48.3	189	6	AAE14830	AAE14830	Human	wil
113	473	52.1	352	5	ABb05344	Human	int	186	438	48.3	189	7	ADN13719	ADN13719	Human	int
114	473	52.1	350	7	ADd69668	Chimeric		187	438	48.3	189	8	ADN10812	ADN10812	Human	int
115	467	51.5	166	8	AAy05808	Human	int	188	438	48.3	189	8	ADs16322	ADs16322	Human	int
116	467	51.5	166	8	AdM79190	Interfero		189	437	48.2	166	3	AAr28177	AAr28177	Chimeric	
117	465	51.3	195	4	AAp60355	Sequence		190	437	48.2	166	4	AAg61794	AAg61794	Interfero	
118	465	51.3	195	4	AAr49781	Human	int	191	437	48.2	166	4	AD129632	AD129632	Human	int
119	465	51.3	195	7	ADf94973	Human	int	192	437	48.2	189	6	ABP70736	ABP70736	Human	int
120	464	51.2	162	2	AAy25093	Human	int	193	436	48.1	166	1	AAp30685	AAp30685	Consensus	
121	461	50.8	195	2	AAw53120	Amino aci		194	436	48.1	170	4	AAr49165	AAr49165	Human	int
122	460.5	50.8	171	1	AAp70332	Sequence		195	436	48.1	189	1	AAp20110	AAp20110	Sequence	
123	459.5	50.7	172	2	AAr24030	Human	int	196	436	48.1	189	1	AAp30230	AAp30230	Sequence	
124	459.5	50.7	172	2	AAr24031	Human	int	197	436	48.1	189	5	ABR07436	ABR07436	Interfero	
125	456	50.3	166	2	AAy05813	Human	int	198	436	48.1	189	8	ADN10810	ADN10810	Human	int
126	456	50.3	166	6	AAg79719	IFN-alpha		199	436	48.1	189	8	ADs16320	ADs16320	Human	int
127	456	50.3	166	8	AdM79187	Interfero		200	435	48.0	166	3	AAr28176	AAr28176	Human	int
128	453	49.9	166	8	AAg61804	Interfero		201	435	48.0	166	4	AAg61814	AAg61814	Interfero	
129	453	49.9	166	8	AD129632	Human	int	202	435	48.0	166	4	AAg61793	AAg61793	Interfero	
130	451	49.7	167	1	AAp70442	Sequence		203	435	48.0	166	8	AD129621	AD129621	Human	int
131	448	49.4	166	2	AAy05807	Human	int	204	435	48.0	166	8	AD129642	AD129642	Human	int
132	448	49.4	166	8	AdM79189	Interfero		205	435	48.0	171	7	ADf47855	ADf47855	Human	alp
133	446	49.2	176	1	AAp60557	Interfero		206	435	48.0	189	5	ABg68069	ABg68069	Human	int
134	445	49.1	182	1	AAp30003	Sequence		207	434	47.9	166	4	AAg61818	AAg61818	Interfero	
135	444	49.0	195	1	AAp60400	Equine IF		208	434	47.9	166	8	AD129646	AD129646	Human	int
136	442	48.7	166	4	AAg61797	Interfero		209	433	47.7	166	2	AAw44105	AAw44105	Chimeric	
137	442	48.7	166	4	AAg61828	Interfero		210	433	47.7	166	4	AAg61802	AAg61802	Interfero	
138	442	48.7	166	5	ABg68078	Human	int	211	433	47.7	166	4	AAg61831	AAg61831	Interfero	
139	442	48.7	166	8	AD129625	Human	int	212	433	47.7	166	4	AAg61832	AAg61832	Interfero	
140	442	48.7	166	8	AD129663	Human	int	213	433	47.7	166	4	AAg61790	AAg61790	Interfero	
141	442	48.7	167	2	AAr11532	Consensus		214	433	47.7	166	4	AAg61823	AAg61823	Interfero	
142	442	48.7	189	5	ABg68070	Human	int	215	433	47.7	166	4	AAg61799	AAg61799	Interfero	
143	441	48.6	166	4	AAg61805	Interfero		216	433	47.7	166	5	ABg68838	ABg68838	Interfero	
144	441	48.6	166	8	AD129633	Human	int	217	433	47.7	166	8	AD129627	AD129627	Human	int
145	440	48.5	166	1	AAp60304	Sequence		218	433	47.7	166	8	AD129651	AD129651	Human	int
146	440	48.5	166	2	AAr67761	Interfero		219	433	47.7	166	8	AD129630	AD129630	Human	int
147	440	48.5	166	4	AAr49160	Human	int	220	433	47.7	166	8	AD129618	AD129618	Human	int
148	440	48.5	166	4	AAg61803	Interfero		221	433	47.7	166	8	AD129666	AD129666	Human	int
149	440	48.5	166	8	AD129631	Interfero		222	433	47.7	166	8	AD129667	AD129667	Human	int
150	440	48.5	166	8	ADL88859	Human	cyt	223	433	47.7	166	8	AD032382	AD032382	Human	int
151	440	48.5	166	8	ADL88853	Human	cyt	224	433	47.7	189	1	AAp10021	AAp10021	Sequence	
152	440	48.5	166	8	AD032377	Human	int	225	432	47.6	166	4	AAr30684	AAr30684	Consensus	
153	440	48.5	167	1	AAp30231	Sequence		226	432	47.6	166	4	AAr49154	AAr49154	Human	int
154	440	48.5	167	1	AAp30224	Sequence		227	432	47.6	166	4	AAg61830	AAg61830	Interfero	
155	440	48.5	167	1	AAp60690	E.coli		228	432	47.6	166	4	AAg61802	AAg61802	Interfero	
156	440	48.5	167	2	AAr07679	IFN-alpha		229	432	47.6	166	8	AD129640	AD129640	Human	int
157	440	48.5	189	2	AAr07678	IFN-alpha		230	432	47.6	166	8	AD129665	AD129665	Human	int
158	440	48.5	189	5	AAW70371	Human	int	231	432	47.6	167	2	AAr11533	AAr11533	Consensus	
159	440	48.5	189	5	ABb07431	Interfero		232	431	47.5	238	4	AAr49159	AAr49159	Human	int
160	440	48.5	189	5	AAg78572	Human	int	233	431	47.5	238	7	ADf94967	ADf94967	Human	int
161	440	48.5	189	6	ABP70735	Human	int	234	430	47.4	167	1	AAp30218	AAp30218	Sequence	
162	440	48.5	189	7	ADG64979	Interfero		235	430	47.4	167	1	AAp60686	AAp60686	Sequence	
163	440	48.5	189	8	ADN10804	Human	int	236	430	47.4	189	1	AAp20106	AAp20106	Sequence	
164	440	48.5	189	8	ADs16314	Human	int	237	430	47.4	189	6	ABP70737	ABP70737	Human	int
165	440	48.5	245	7	AAr49778	Human	int	238	429	47.3	166	4	AAr49159	AAr49159	Human	int
166	438	48.3	166	4	AAr49167	Human	int	239	429	47.3	166	4	AAr49164	AAr49164	Human	int
167	438	48.3	166	4	AAr49167	Human	int	240	429	47.3	166	4	AAg61796	AAg61796	Interfero	
168	438	48.3	166	4	AAg61819	Interfero		241	429	47.3	166	8	AD129624	AD129624	Human	int
169	438	48.3	166	4	AAg61792	Interfero		242	429	47.3	166	8	ADL88856	ADL88856	Human	cyt
170	438	48.3	166	4	AAg61824	Interfero		243	429	47.3	166	8	ADL88849	ADL88849	Human	int
171	438	48.3	166	4	AAg61795	Interfero		244	429	47.3	166	8	AD032381	AD032381	Human	int

245	429	47.3	166	8	ADO32376	Ado32376	Human	int	318	424	46.7	166	4	AAAG61817	Aag61817	Interfero
246	429	47.3	167	1	AAp30229	Aap30229	Sequence		319	424	46.7	166	8	AD129645	Ad129645	Human
247	429	47.3	167	1	AAp80046	Aap80046	Sequence		320	424	46.7	166	8	ADO32445	Ado32445	Human
248	429	47.3	189	1	AAp20105	Aap20105	Sequence		321	424	46.7	166	8	ADO32351	Ado32351	Human
249	429	47.3	189	1	AAp30228	Aap30228	Sequence		322	424	46.7	167	1	AAp40129	Aap40129	Sequence
250	429	47.3	189	5	ABBo7432	Abbo7432	Interfero		323	424	46.7	189	5	ABG68061	Abg68061	Human
251	429	47.3	189	5	ABBo7438	Abbo7438	Interfero		324	423	46.6	166	1	AAp60828	Aap60828	Sequence
252	429	47.3	189	5	AAg78566	Aag78566	Human	int	325	423	46.6	166	4	AAg61811	Aag61811	Interfero
253	429	47.3	189	5	AAg78568	Aag78568	Human	int	326	423	46.6	166	8	AD129639	Ad129639	Human
254	429	47.3	189	8	ADN10808	Adn10808	Human	int	327	423	46.6	166	8	ADO32447	Ado32447	Human
255	429	47.3	189	8	ADSL16318	Adsl16318	Human	int	328	423	46.6	189	1	AAp30165	Aap30165	Sequence
256	428	47.2	166	1	AAp50229	Aap50229	Interfero		329	423	46.6	189	4	AAp49779	Aap49779	Human
257	428	47.2	166	2	AAr42813	Aar42813	Lymphobla		330	422	46.6	189	7	ADP94971	Adp94971	Human
258	428	47.2	166	2	AAW43380	Aaw43380	Human	int	331	422	46.5	166	4	AAg61810	Aag61810	Interfero
259	428	47.2	166	3	AABo7339	Aabo7339	Matucre	hu	332	422	46.5	166	4	AAg61826	Aag61826	Interfero
260	428	47.2	166	3	AAy44831	Aay44831	Hybrid	in	333	422	46.5	166	4	AAg61816	Aag61816	Interfero
261	428	47.2	166	3	AAAB12968	Aaab12968	Human	int	334	422	46.5	166	4	AAE11365	Aae11365	Human
262	428	47.2	166	4	AAAB49157	Aaab49157	Human	int	335	422	46.5	166	5	ABG68077	Abg68077	Human
263	428	47.2	166	4	AAAG61800	Aag61800	Interfero		336	422	46.5	166	8	AD129661	Ad129661	Human
264	428	47.2	166	4	AAAG61815	Aag61815	Interfero		337	422	46.5	166	8	AD129644	Ad129644	Human
265	428	47.2	166	5	AAm50694	Aam50694	Human	mat	338	422	46.5	166	8	AD129638	Ad129638	Human
266	428	47.2	166	5	ABG68055	Abg68055	Rhesus	in	339	422	46.5	166	8	ADO32430	Ado32430	Human
267	428	47.2	166	6	AAg79717	Aag79717	Human	IFN	340	422	46.5	189	2	AAp64240	Aap64240	Human
268	428	47.2	166	7	ADP70841	Adp70841	Human	alp	341	422	46.5	189	2	AAW62452	Aaw62452	Human
269	428	47.2	166	8	AD128137	Ad128137	Human	int	342	422	46.5	189	2	AAW94083	Aaw94083	Human
270	428	47.2	166	8	AD129628	Ad129628	Human	int	343	422	46.5	189	3	AAy59395	Aay59395	Human
271	428	47.2	166	8	AD129643	Ad129643	Human	int	344	422	46.5	189	4	AAE14364	Aae14364	Human
272	428	47.2	166	8	AD192171	Ad192171	Interfero		345	422	46.5	189	5	ABG68075	Abg68075	Human
273	428	47.2	166	8	ADL88852	Adl88852	Human	cyt	346	422	46.5	189	5	ABG68059	Abg68059	Human
274	428	47.2	166	8	ADM79184	Adm79184	Matucre	hu	347	422	46.5	189	8	ADG32291	Adg32291	Human
275	428	47.2	166	8	ADP23374	Adp23374	Human	int	348	421	46.4	166	4	AAp49168	Aap49168	Human
276	428	47.2	167	1	AAp20113	Aap20113	Human	int	349	421	46.4	166	4	AAg61827	Aag61827	Interfero
277	428	47.2	167	1	AAp30185	Aap30185	Sequence		350	421	46.4	166	8	AD129662	Ad129662	Human
278	428	47.2	167	1	AAp80052	Aap80052	Sequence		351	421	46.4	166	8	ADL88860	Adl88860	Human
279	428	47.2	188	1	AAp20013	Aap20013	Hybrid	hu	352	421	46.4	166	8	ADG22353	Adg22353	Human
280	428	47.2	189	1	AAp10020	Aap10020	Sequence		353	421	46.4	166	8	ADG23385	Adg23385	Human
281	428	47.2	189	1	AAp20111	Aap20111	Sequence		354	421	46.4	181	8	ADG88033	Adg88033	Tumour
282	428	47.2	189	1	AAp30182	Aap30182	Sequence		355	421	46.4	187	2	AAp62368	Aap62368	Interfero
283	428	47.2	189	1	AAp40126	Aap40126	Sequence		356	421	46.4	189	5	ABG68066	Abg68066	Human
284	428	47.2	189	2	AAW53119	Aaw53119	Amiino	aci	357	420	46.3	166	3	AAy44829	Aay44829	Hybrid
285	428	47.2	189	2	AAy22636	Aay22636	Human	int	358	420	46.3	166	8	ADO32432	Ado32432	Human
286	428	47.2	189	3	AAAB12967	Aaab12967	Human	int	359	420	46.3	188	1	AAp20009	Aap20009	Hybrid
287	428	47.2	189	5	AAE15827	Aae15827	Human	int	360	420	46.3	189	5	ABG68067	Abg68067	Human
288	428	47.2	189	5	ABG68062	Abg68062	Human	int	361	419	46.2	166	3	AAy44832	Aay44832	Mutant
289	428	47.2	189	5	ABBo7437	Abbo7437	Interfero		362	419	46.2	166	3	AAy44833	Aay44833	Hybrid
290	428	47.2	189	5	AAg78564	Aag78564	Human	int	363	419	46.2	166	4	AAg61791	Aag61791	Interfero
291	428	47.2	189	7	ADG78899	Adg78899	Human	PRO	364	419	46.2	166	4	AAg61829	Aag61829	Interfero
292	428	47.2	189	7	ABU64301	Abu64301	Human	int	365	419	46.2	166	4	AAg61806	Aag61806	Interfero
293	428	47.2	189	8	ADN10800	Adn10800	Human	int	366	419	46.2	166	8	AD129619	Ad129619	Human
294	428	47.2	189	8	ADN10809	Adn10809	Human	int	367	419	46.2	166	8	AD129634	Ad129634	Human
295	428	47.2	189	8	ADSL16310	Adsl16310	Human	int	368	419	46.2	166	8	AD129664	Ad129664	Human
296	428	47.2	189	8	ADSL16319	Adsl16319	Human	int	369	419	46.2	166	8	ADO32352	Ado32352	Human
297	427.5	47.1	185	8	ADL88898	Adl88898	Human	cyt	370	419	46.2	188	1	AAp20010	Aap20010	Hybrid
298	426	47.0	166	1	AAp30686	Aap30686	Consensus		371	419	46.2	189	1	AAp20108	Aap20108	Sequence
299	426	47.0	166	5	ABG68079	Abg68079	Human	int	372	419	46.2	189	2	AAp07680	Aap07680	IFN-alpha
300	426	47.0	167	1	AAp40180	Aap40180	Sequence		373	419	46.2	189	4	AAp49780	Aap49780	Human
301	426	47.0	189	1	AAp40179	Aap40179	Sequence		374	419	46.2	189	5	AAU84283	Aau84283	Human
302	425	46.9	166	2	AAr67762	Aar67762	Interfero		375	419	46.2	189	5	ABG68076	Abg68076	Human
303	425	46.9	166	4	AAg78111	Aag78111	Human	int	376	419	46.2	189	5	ABG68072	Abg68072	Human
304	425	46.9	166	4	AAAG61808	Aag61808	Interfero		377	419	46.2	189	5	ABG68071	Abg68071	Human
305	425	46.9	166	4	AAAG61798	Aag61798	Interfero		378	419	46.2	189	5	ABBo7433	Abbo7433	Human
306	425	46.9	166	5	ABG68081	Abg68081	Human	int	379	419	46.2	189	5	AAg78570	Aag78570	Human
307	425	46.9	166	8	AD129636	Ad129636	Human	int	380	419	46.2	189	7	ABB98719	Abb98719	Human
308	425	46.9	166	8	AD129626	Ad129626	Human	int	381	419	46.2	189	6	ADP94972	Adp94972	Human
309	425	46.9	166	8	ADL88855	Adl88855	Human	cyt	382	419	46.2	189	8	ADN10813	Adn10813	Human
310	425	46.9	167	2	AAp07681	Aap07681	IFN-alpha		383	419	46.2	189	8	ADN16323	Adn16323	Human
311	425	46.9	189	1	AAp30101	Aap30101	Sequence		384	418	46.1	166	4	AAg61807	Aag61807	Interfero
312	425	46.9	189	1	AAp50306	Aap50306	Human	int	385	418	46.1	166	8	AD129635	Ad129635	Human
313	425	46.9	189	2	AAW70373	Aaw70373	Human	int	386	417	46.0	165	1	AAp30687	Aap30687	Hybrid
314	425	46.9	189	5	ABG68068	Abg68068	Human	int	387	417	46.0	166	8	ADO32354	Ado32354	Human
315	425	46.9	189	5	ABG68065	Abg68065	Human	int	388	417	46.0	166	8	ADO32436	Ado32436	Human
316	425	46.9	189	8	ADN10803	Adn10803	Human	int	389	416	45.9	166	4	AAg61821	Aag61821	Interfero
317	425	46.9	189	8	ADSL16313	Adsl16313	Human	int	390	416	45.9	166	5	ABG68080	Abg68080	Human

391	416	45.9	166	8	AD129649	Ad129649 Human int	464	408	45.0	167	1	AAp60320	AAp60320 Sequence
392	416	45.9	166	8	AD032355	Ad032355 Human int	465	408	45.0	164	1	AAp60399	AAp60399 Equine IF
393	416	45.9	166	8	AD032433	Ad032433 Human IFN	466	407.5	44.9	162	1	AAp50168	AAp50168 Sequence
394	416	45.9	166	8	AD032442	Ad032442 Human IFN	467	407.5	44.9	165	7	ADP16224	ADP16224 Human alb
395	416	45.9	167	1	AAp30184	AAp30184 Sequence	468	407.5	44.9	165	7	ADP16244	ADP16244 Human alb
396	416	45.9	167	1	AAp40128	AAp40128 Sequence	469	407.5	44.9	165	7	ADH21660	ADH21660 Human IFN
397	416	45.9	171	7	ADP30369	ADP30369 Recombina	470	407.5	44.9	165	7	ADH21680	ADH21680 Human IFN
398	416	45.9	189	1	AAp30179	AAp30179 Sequence	471	407.5	44.9	396	8	ADP49583	ADP49583 Human IGG
399	416	45.9	189	1	AAp30164	AAp30164 Sequence	472	407.5	44.9	774	7	ADP16222	ADP16222 Human alb
400	416	45.9	189	1	AAp40123	AAp40123 Sequence	473	407.5	44.9	774	7	ADH21658	ADH21658 Human alb
401	415	45.8	166	3	AAy44974	AAy44974 Human hyb	474	407	44.9	166	3	AAAB07338	AAAB07338 Mature hu
402	415	45.8	166	3	AAy44826	AAy44826 Hybrid in	475	407	44.9	166	8	AD032346	AD032346 Human int
403	415	45.8	166	4	AAAG61813	AAAG61813 Interfero	476	407	44.9	166	8	AD032441	AD032441 Human IFN
404	415	45.8	166	5	ABG68085	ABG68085 Rhesus in	477	407	44.9	166	8	AD032393	AD032393 Human IFN
405	415	45.8	166	5	ABG68082	ABG68082 Human int	478	407	44.9	167	1	AAp60317	AAp60317 Sequence
406	415	45.8	166	5	ABG68057	ABG68057 Rhesus in	479	407	44.9	167	8	AD032388	AD032388 Human IFN
407	415	45.8	166	8	AD129641	Ad129641 Human int	480	406.5	44.8	168	1	AAp60318	AAp60318 Sequence
408	415	45.8	166	8	AD032444	Ad032444 Human IFN	481	406.5	44.8	774	7	ADP16242	ADP16242 Human alb
409	415	45.8	166	8	AD032350	Ad032350 Human IFN	482	406.5	44.8	162	5	ADH21678	ADH21678 Human alb
410	414.5	45.7	165	2	AAy43492	AAy43492 A human i	483	406	44.8	162	5	ABG68845	ABG68845 Interfero
411	414.5	45.7	165	3	AAy82887	AAy82887 N-termina	484	406	44.8	166	1	AAp90189	AAp90189 Hybrid al
412	414.5	45.7	166	2	AAy43491	AAy43491 A human i	485	406	44.8	166	3	AAAB07344	AAAB07344 Mature hu
413	414.5	45.7	166	3	AAy82805	AAy82805 N-termina	486	406	44.8	166	3	AAAB07350	AAAB07350 Mature mu
414	414.5	45.7	166	3	AAy82886	AAy82886 Interfero	487	406	44.8	166	5	ABG68839	ABG68839 Interfero
415	414.5	45.7	167	3	AAy82804	AAy82804 Interfero	488	406	44.8	166	8	AD032397	AD032397 Human IFN
416	414.5	45.7	274	2	AAy02097	AAy02097 A multifu	489	405	44.8	198	6	ABP56433	ABP56433 Interfero
417	414.5	45.7	274	2	AAy02092	AAy02092 A multifu	490	405	44.7	166	1	AAp60104	AAp60104 Sequence
418	414.5	45.7	453	2	AAy02093	AAy02093 A multifu	491	405	44.7	166	1	AAp90190	AAp90190 Hybrid al
419	414.5	45.7	453	2	AAy02099	AAy02099 A multifu	492	405	44.7	166	2	AAAR42814	AAAR42814 Lymphobla
420	414.5	45.7	470	2	AAy02112	AAy02112 A multifu	493	405	44.7	166	2	AAAR70088	AAAR70088 Recombina
421	414	45.6	166	8	AD032426	Ad032426 Human IFN	494	405	44.7	166	2	AAW05337	AAW05337 Alpha-int
422	414	45.6	166	8	AD032446	Ad032446 Human IFN	495	405	44.7	166	3	AAAB07341	AAAB07341 Mature hu
423	414	45.6	165	3	AAy03357	AAy03357 Human int	496	405	44.7	166	4	AAAB49162	AAAB49162 Human int
424	413.5	45.6	165	3	AAy44976	AAy44976 Human hyb	497	405	44.7	166	8	ADL88858	ADL88858 Human cyt
425	413.5	45.6	165	3	AAy44828	AAy44828 Hybrid in	498	405	44.7	166	8	AD032429	AD032429 Human IFN
426	413	45.5	166	1	AAp30683	AAp30683 Synthetic	499	405	44.7	166	8	AD032389	AD032389 Human IFN
427	413	45.5	166	5	ABG68054	ABG68054 Rhesus in	500	405	44.7	166	8	AD032427	AD032427 Human IFN
428	413	45.5	166	5	ABG68058	ABG68058 Rhesus in	501	405	44.7	166	8	AD032379	AD032379 Human int
429	413	45.5	166	8	AD032437	Ad032437 Human IFN	502	405	44.7	166	8	AD032345	AD032345 Human int
430	413	45.5	166	8	AD032443	Ad032443 Human IFN	503	405	44.7	167	1	AAp60222	AAp60222 Sequence
431	412.5	45.5	150	2	AAAR1799	AAAR1799 Interfero	504	405	44.7	167	1	AAp60316	AAp60316 Sequence
432	412.5	45.5	165	7	ADP16239	ADP16239 Human alb	505	405	44.7	167	2	AAW05336	AAW05336 Alpha-int
433	412.5	45.5	165	7	ADH21675	ADH21675 Human IFN	506	405	44.7	189	1	AAp20112	AAp20112 Sequence
434	412.5	45.5	774	7	ADP16237	ADP16237 Human alb	507	405	44.7	189	5	ABBO74429	ABBO74429 Interfero
435	412.5	45.5	774	7	ADH21673	ADH21673 Human alb	508	405	44.7	189	5	AAg78569	AAg78569 Human int
436	412	45.4	166	1	AAp60101	AAp60101 Sequence	509	405	44.7	189	6	AAO27034	AAO27034 Human int
437	412	45.4	166	1	AAp90187	AAp90187 Hybrid al	510	404.5	44.6	165	3	AAy44977	AAy44977 Human hyb
438	412	45.4	166	8	AD032348	Ad032348 Human int	511	404.5	44.6	165	8	ADL80663	ADL80663 Human mut
439	412	45.4	166	8	AD032356	Ad032356 Human IFN	512	404.5	44.6	165	8	ADL88833	ADL88833 Human mod
440	412	45.4	166	8	AD032439	Ad032439 Human IFN	513	404	44.5	166	3	AAy44983	AAy44983 Human mut
441	412	45.4	167	1	AAp60315	AAp60315 Sequence	514	404	44.5	166	3	AAy44979	AAy44979 Human hyb
442	412	45.4	167	1	AAp60314	AAp60314 Sequence	515	404	44.5	166	3	AAy44982	AAy44982 Human mut
443	412	45.4	189	5	ABG68063	ABG68063 Human int	516	404	44.5	166	3	AAAB07346	AAAB07346 Mature hu
444	411	45.3	166	8	AD032431	Ad032431 Human IFN	517	404	44.5	166	3	AAy44834	AAy44834 Mutant hu
445	411	45.3	166	8	AD032434	Ad032434 Human IFN	518	404	44.5	166	3	AAy44835	AAy44835 Mutant hy
446	411	45.3	167	1	AAp70333	AAp70333 Sequence	519	404	44.5	166	4	AAAG61801	AAAG61801 Interfero
447	410	45.2	166	1	AAp60103	AAp60103 Sequence	520	404	44.5	166	8	AD129629	AD129629 Human int
448	410	45.2	166	3	AAAB07343	AAAB07343 Mutant hu	521	404	44.5	166	8	ADN10806	ADN10806 Human int
449	410	45.2	166	4	AAAG61820	AAAG61820 Interfero	522	404	44.5	189	8	AD016316	AD016316 Human int
450	410	45.2	166	8	AD129648	Ad129648 Human int	523	403.5	44.5	165	3	AAy44981	AAy44981 Human mut
451	410	45.2	166	8	AD032349	Ad032349 Human int	524	403.5	44.5	165	3	AAy44980	AAy44980 Human mut
452	409	45.1	166	8	AD032435	Ad032435 Human IFN	525	403	44.4	166	1	AAp60102	AAp60102 Sequence
453	409	45.1	166	8	AD032358	Ad032358 Human int	526	403	44.4	166	1	AAp90188	AAp90188 Hybrid al
454	409	45.1	166	8	AD032440	Ad032440 Human IFN	527	403	44.4	166	3	AAy44978	AAy44978 Human hyb
455	409	45.1	171	1	AAp60764	AAp60764 Plasmid e	528	403	44.4	166	3	AAAB07342	AAAB07342 Mutant hu
456	408.5	45.0	165	7	ADP16234	ADP16234 Human alb	529	403	44.4	166	3	AAy44830	AAy44830 Hybrid in
457	408.5	45.0	165	7	ADH21670	ADH21670 Human IFN	530	403	44.4	166	8	AD032428	AD032428 Human IFN
458	408.5	45.0	774	7	ADP16232	ADP16232 Human alb	531	403	44.4	166	8	AD032438	AD032438 Human IFN
459	408.5	45.0	774	7	ADH21668	ADH21668 Human alb	532	403	44.4	184	1	AAp61360	AAp61360 Equine in
460	408	45.0	166	3	AAy53126	AAy53126 Human int	533	402.5	44.4	184	1	AAp60397	AAp60397 Equine IF
461	408	45.0	166	3	AAy44975	AAy44975 Human hyb	534	402.5	44.4	165	7	ADP16229	ADP16229 Human alb
462	408	45.0	166	3	AAy44827	AAy44827 Hybrid in	535	402.5	44.4	165	7	ADH21665	ADH21665 Human IFN
463	408	45.0	166	8	AD032347	Ad032347 Human IFN	536	402.5	44.4	165	8	ADL90662	ADL90662 Human mut

537	402.5	44.4	165	8	ADL90622	Adl190622	Human	mut	610	398.5	43.9	165	8	ADL99645	Adl199645	Human	mod
538	402.5	44.4	165	8	ADL88792	Adl188792	Human	mod	611	398.5	43.9	165	8	ADL88699	Adl188699	Human	mod
539	402.5	44.4	165	8	ADL88832	Adl188832	Human	mod	612	398.5	43.9	165	8	ADL88747	Adl188747	Human	mod
540	402.5	44.4	396	8	ADL84585	Adl184585	Human	IGG	613	398.5	43.9	165	8	ADL88723	Adl188723	Human	mod
541	402.5	44.4	753	2	AAV02095	AAV02095	A	multifu	614	398.5	43.9	165	8	ADL88775	Adl188775	Human	mod
542	402.5	44.4	774	7	ADL16227	Adl16227	Human	alb	615	398.5	43.9	165	8	ADL88698	Adl188698	Human	mod
543	402.5	44.4	774	7	ADH21663	Adh21663	Human	alb	616	398.5	43.9	165	8	ADL88774	Adl188774	Human	mod
544	402	44.3	166	3	AAH07347	AAh07347	Mutant	hu	617	398.5	43.9	165	8	ADL89969	Adl189969	Human	mod
545	401.5	44.3	165	8	ADL90581	Adl190581	Human	mut	618	398.5	43.9	165	8	ADL88668	Adl188668	Human	mod
546	401.5	44.3	165	8	ADL90606	Adl190606	Human	mut	619	398.5	43.9	165	8	ADL88795	Adl188795	Human	mod
547	401.5	44.3	165	8	ADL90668	Adl190668	Human	mut	620	398.5	43.9	165	8	ADL94917	Adl184917	Human	int
548	401.5	44.3	165	8	ADL90533	Adl190533	Human	mut	621	398.5	43.9	165	8	ADL94914	Adl184914	Human	int
549	401.5	44.3	165	8	ADL88703	Adl188703	Human	mod	622	398.5	43.9	165	8	ADL94951	Adl184951	Human	IGG
550	401.5	44.3	165	8	ADL88751	Adl188751	Human	mod	623	398.5	43.9	165	8	ADL94958	Adl184958	Human	IGG
551	401.5	44.3	165	8	ADL88838	Adl188838	Human	mod	624	398	43.9	102	2	AAW09282	AAW09282	Human	mat
552	401.5	44.3	165	8	ADL88776	Adl188776	Human	mod	625	398	43.9	102	2	AAW44114	AAW44114	Human	int
553	401.5	44.3	396	8	ADL94586	Adl194586	Human	IGG	626	398	43.9	164	8	ADL902425	ADL902425	Human	IGG
554	401	44.2	166	3	AAH07345	AAh07345	Mutant	hu	627	398	43.9	166	1	AAW04210	AAW04210	Novel	int
555	401	44.2	166	3	AAH07349	AAh07349	Mutant	hu	628	398	43.9	166	1	AAW04210	AAW04210	Novel	int
556	401	44.2	166	8	ADL90398	Adl190398	Human	IFN	629	398	43.9	166	2	AAW20053	AAW20053	Human	IFN
557	401	44.2	166	8	ADL903412	Adl1903412	Human	IFN	630	398	43.9	166	4	AAW49166	AAW49166	Human	int
558	400.5	44.2	165	2	AAW43384	AAW43384	Human	int	631	398	43.9	166	8	ADL903283	ADL903283	Human	int
559	400.5	44.2	165	8	ADL90598	Adl190598	Human	mut	632	398	43.9	166	8	ADL9032424	ADL9032424	Human	IFN
560	400.5	44.2	165	8	ADL90542	Adl190542	Human	mut	633	398	43.9	166	8	ADL9032387	ADL9032387	Human	IFN
561	400.5	44.2	165	8	ADL90506	Adl190506	Human	mut	634	398	43.9	189	1	AAW50104	AAW50104	Sequence	
562	400.5	44.2	165	8	ADL88712	Adl188712	Human	mod	635	398	43.9	189	5	ABH07435	ABH07435	Interfero	
563	400.5	44.2	165	8	ADL88768	Adl188768	Human	mod	636	398	43.9	189	5	AAW78571	AAW78571	Human	int
564	400.5	44.2	165	8	ADL88676	Adl188676	Human	mod	637	398	43.9	189	8	ADL10811	ADL10811	Human	int
565	400.5	44.2	165	8	ADL88851	Adl188851	Human	cyt	638	398	43.9	189	1	ADL16321	ADL16321	Human	int
566	400.5	44.2	165	8	ADL94615	Adl194615	Human	int	639	397.5	43.8	165	1	AAW50228	AAW50228	Interfero	
567	400.5	44.2	166	1	AAW70329	AAW70329	Sequence		640	397.5	43.8	165	2	AAW62234	AAW62234	Recombina	
568	400.5	44.2	188	2	AAW20564	AAW20564	O-Glycosy		641	397.5	43.8	165	2	AAW14015	AAW14015	Interfero	
569	400.5	44.2	188	2	AAW20549	AAW20549	Human	IFN	642	397.5	43.8	165	2	AAW43379	AAW43379	Human	int
570	400.5	44.2	188	2	AAW66199	AAW66199	E. coli	ST	643	397.5	43.8	165	2	AAW02090	AAW02090	A multifu	
571	400.5	44.2	396	8	ADL94587	Adl194587	Human	IGG	644	397.5	43.8	165	2	AAW02091	AAW02091	A multifu	
572	400.5	44.2	396	8	ADL94584	Adl194584	Human	IGG	645	397.5	43.8	165	2	AAW43488	AAW43488	A human i	
573	400	44.1	166	3	AAH07348	AAh07348	Mutant	hu	646	397.5	43.8	165	2	AAW43489	AAW43489	A human i	
574	400	44.1	166	8	ADL903344	Adl1903344	Human	int	647	397.5	43.8	165	2	AAW43490	AAW43490	A human i	
575	400	44.1	433	2	AAW18579	AAW18579	Interfero		648	397.5	43.8	165	3	AAW82884	AAW82884	Interfero	
576	399.5	44.0	165	4	AAW06746	AAW06746	Human	int	649	397.5	43.8	165	3	AAW82885	AAW82885	N-termina	
577	399.5	44.0	165	8	ADL90517	Adl190517	Human	mut	650	397.5	43.8	165	3	AAW82883	AAW82883	Interfero	
578	399.5	44.0	165	8	ADL90565	Adl190565	Human	mut	651	397.5	43.8	165	5	AAW50705	AAW50705	Human	mat
579	399.5	44.0	165	8	ADL90558	Adl190558	Human	mut	652	397.5	43.8	165	5	AAW50693	AAW50693	Human	mat
580	399.5	44.0	165	8	ADL90596	Adl190596	Human	mut	653	397.5	43.8	165	5	AAW18958	AAW18958	Human	alp
581	399.5	44.0	165	8	ADL90599	Adl190599	Human	mut	654	397.5	43.8	165	7	ADL98104	ADL98104	Human	int
582	399.5	44.0	165	8	ADL90499	Adl190499	Human	mut	655	397.5	43.8	165	7	ADL915325	ADL915325	Human	alb
583	399.5	44.0	165	8	ADL90502	Adl190502	Human	mut	656	397.5	43.8	165	7	ADL915304	ADL915304	Human	alb
584	399.5	44.0	165	8	ADL88728	Adl188728	Human	mod	657	397.5	43.8	165	7	ADL915270	ADL915270	Human	alb
585	399.5	44.0	165	8	ADL88769	Adl188769	Human	mod	658	397.5	43.8	165	7	ADL916215	ADL916215	Human	alb
586	399.5	44.0	165	8	ADL88735	Adl188735	Human	mod	659	397.5	43.8	165	7	ADL915320	ADL915320	Human	alb
587	399.5	44.0	165	8	ADL88766	Adl188766	Human	mod	660	397.5	43.8	165	7	ADL915321	ADL915321	Human	alb
588	399.5	44.0	165	8	ADL88669	Adl188669	Human	mod	661	397.5	43.8	165	7	ADL915315	ADL915315	Human	alb
589	399.5	44.0	165	8	ADL88687	Adl188687	Human	mod	662	397.5	43.8	165	7	ADL907840	ADL907840	Human	alp
590	399.5	44.0	165	8	ADL88672	Adl188672	Human	mod	663	397.5	43.8	165	7	ADL913397	ADL913397	Human	int
591	399	44.0	184	1	AAW60404	AAW60404	Equine	IF	664	397.5	43.8	165	7	ADL914400	ADL914400	Human	int
592	399	44.0	189	5	AAW81097	AAW81097	Porcine	I	665	397.5	43.8	165	7	ADL913387	ADL913387	Human	int
593	399	44.0	189	6	AAW98720	AAW98720	Human	alp	666	397.5	43.8	165	7	ADL912657	ADL912657	Human	IFN
594	398.5	43.9	165	8	ADL90624	Adl190624	Human	mut	667	397.5	43.8	165	7	ADL912375	ADL912375	Human	int
595	398.5	43.9	165	8	ADL90577	Adl190577	Human	mut	668	397.5	43.8	165	7	ADL912396	ADL912396	Human	int
596	398.5	43.9	165	8	ADL90633	Adl190633	Human	mut	669	397.5	43.8	165	7	ADL912392	ADL912392	Human	int
597	398.5	43.9	165	8	ADL90528	Adl190528	Human	mut	670	397.5	43.8	165	7	ADL90497	ADL90497	Human	int
598	398.5	43.9	165	8	ADL90605	Adl190605	Human	mut	671	397.5	43.8	165	8	ADL90626	ADL90626	Human	mut
599	398.5	43.9	165	8	ADL90529	Adl190529	Human	mut	672	397.5	43.8	165	8	ADL90588	ADL90588	Human	mut
600	398.5	43.9	165	8	ADL90553	Adl190553	Human	mut	673	397.5	43.8	165	8	ADL90568	ADL90568	Human	mut
601	398.5	43.9	165	8	ADL90669	Adl190669	Human	mut	674	397.5	43.8	165	8	ADL90559	ADL90559	Human	mut
602	398.5	43.9	165	8	ADL90498	Adl190498	Human	mut	675	397.5	43.8	165	8	ADL90623	ADL90623	Human	mut
603	398.5	43.9	165	8	ADL90604	Adl190604	Human	mut	676	397.5	43.8	165	8	ADL90670	ADL90670	Human	mut
604	398.5	43.9	165	8	ADL90694	Adl190694	Human	mut	677	397.5	43.8	165	8	ADL90501	ADL90501	Human	mut
605	398.5	43.9	165	8	ADL90692	Adl190692	Human	mut	678	397.5	43.8	165	8	ADL90593	ADL90593	Human	mut
606	398.5	43.9	165	8	ADL90625	Adl190625	Human	mut	679	397.5	43.8	165	8	ADL90511	ADL90511	Human	mut
607	398.5	43.9	165	8	ADL88803	Adl188803	Human	mod	680	397.5	43.8	165	8	ADL90574	ADL90574	Human	mut
608	398.5	43.9	165	8	ADL88839	Adl188839	Human	mod	681	397.5	43.8	165	8	ADL90603	ADL90603	Human	mut
609	398.5	43.9	165	8	ADL88794	Adl188794	Human	mod	682	397.5	43.8	165	8	ADL90503	ADL90503	Human	mut

683	397.5	43.8	165	8	ADL90597	Adl90597	Human	mut	756	396.5	43.7	165	8	ADL90505	Adl90505	Human	mut
684	397.5	43.8	165	8	ADL90620	Adl90620	Human	mut	757	396.5	43.7	165	8	ADL90557	Adl90557	Human	mut
685	397.5	43.8	165	8	ADL90612	Adl90612	Human	mut	758	396.5	43.7	165	8	ADL90575	Adl90575	Human	mut
686	397.5	43.8	165	8	ADL90602	Adl90602	Human	mut	759	396.5	43.7	165	8	ADL90615	Adl90615	Human	mut
687	397.5	43.8	165	8	ADL88763	Adl88763	Human	mod	760	396.5	43.7	165	8	ADL90671	Adl90671	Human	mut
688	397.5	43.8	165	8	ADL88729	Adl88729	Human	mod	761	396.5	43.7	165	8	ADL90672	Adl90672	Human	mut
689	397.5	43.8	165	8	ADL88681	Adl88681	Human	mod	762	396.5	43.7	165	8	ADL90508	Adl90508	Human	mut
690	397.5	43.8	165	8	ADL88667	Adl88667	Human	cyt	763	396.5	43.7	165	8	ADL90549	Adl90549	Human	mut
691	397.5	43.8	165	8	ADL88790	Adl88790	Human	mod	764	396.5	43.7	165	8	ADL90589	Adl90589	Human	mut
692	397.5	43.8	165	8	ADL88837	Adl88837	Human	mod	765	396.5	43.7	165	8	ADL90702	Adl90702	Human	mut
693	397.5	43.8	165	8	ADL88782	Adl88782	Human	mod	766	396.5	43.7	165	8	ADL90627	Adl90627	Human	mut
694	397.5	43.8	165	8	ADL88758	Adl88758	Human	mod	767	396.5	43.7	165	8	ADL90531	Adl90531	Human	mut
695	397.5	43.8	165	8	ADL88793	Adl88793	Human	mod	768	396.5	43.7	165	8	ADL90655	Adl90655	Human	mut
696	397.5	43.8	165	8	ADL88840	Adl88840	Human	mod	769	396.5	43.7	165	8	ADL90700	Adl90700	Human	mut
697	397.5	43.8	165	8	ADL88673	Adl88673	Human	mod	770	396.5	43.7	165	8	ADL90563	Adl90563	Human	mut
698	397.5	43.8	165	8	ADL88738	Adl88738	Human	mod	771	396.5	43.7	165	8	ADL90595	Adl90595	Human	mut
699	397.5	43.8	165	8	ADL88772	Adl88772	Human	mod	772	396.5	43.7	165	8	ADL90664	Adl90664	Human	mut
700	397.5	43.8	165	8	ADL88744	Adl88744	Human	mod	773	396.5	43.7	165	8	ADL88678	Adl88678	Human	mod
701	397.5	43.8	165	8	ADL88767	Adl88767	Human	mod	774	396.5	43.7	165	8	ADL88825	Adl88825	Human	mod
702	397.5	43.8	165	8	ADL88796	Adl88796	Human	mod	775	396.5	43.7	165	8	ADL88834	Adl88834	Human	mod
703	397.5	43.8	165	8	ADL88773	Adl88773	Human	mod	776	396.5	43.7	165	8	ADL88675	Adl88675	Human	mod
704	397.5	43.8	165	8	ADL88671	Adl88671	Human	mod	777	396.5	43.7	165	8	ADL88785	Adl88785	Human	mod
705	397.5	43.8	165	8	AD032375	Ado32375	Human	mod	778	396.5	43.7	165	8	ADL88797	Adl88797	Human	mod
706	397.5	43.8	165	8	ADSL17969	Adsl17969	Human	int	779	396.5	43.7	165	8	ADL88842	Adl88842	Human	mod
707	397.5	43.8	165	8	ADRA49576	Adra49576	Human	int	780	396.5	43.7	165	8	ADL88733	Adl88733	Human	mod
708	397.5	43.8	166	1	AAPE00114	Aape00114	Human	int	781	396.5	43.7	165	8	ADL88701	Adl88701	Human	mod
709	397.5	43.8	166	2	AAW05039	Aaw05039	Sequence		782	396.5	43.7	165	8	ADL88745	Adl88745	Human	mod
710	397.5	43.8	166	2	AAW05040	Aaw05040	Protein #		783	396.5	43.7	165	8	ADL88841	Adl88841	Human	mod
711	397.5	43.8	166	3	AAW05040	Aaw05040	Protein #		784	396.5	43.7	165	8	ADL89653	Adl89653	Human	mod
712	397.5	43.8	166	3	AAW82803	Aaw82803	N-termIna		785	396.5	43.7	165	8	ADL88719	Adl88719	Human	mod
713	397.5	43.8	166	4	AAAG65241	Aaag65241	Human	alp	786	396.5	43.7	165	8	ADL88765	Adl88765	Human	mod
714	397.5	43.8	166	5	AAU98666	Aau98666	Human	int	787	396.5	43.7	165	8	ADL89651	Adl89651	Human	mod
715	397.5	43.8	166	8	ADN10802	Adn10802	Human	int	788	396.5	43.7	165	8	ADL88727	Adl88727	Human	mod
716	397.5	43.8	166	8	AD081955	Adq81955	Human	int	789	396.5	43.7	165	8	ADL88759	Adl88759	Human	mod
717	397.5	43.8	166	8	ADSL6312	Adsl6312	Human	int	790	396	43.7	164	8	AD032409	Ado32409	Human	IFN
718	397.5	43.8	167	3	AAV82802	Aav82802	Interfero		791	396	43.7	166	8	AD032396	Ado32396	Human	IFN
719	397.5	43.8	167	3	AAV82801	Aav82801	Interfero		792	396	43.7	166	8	AD032411	Ado32411	Human	IFN
720	397.5	43.8	182	1	AAPI0018	Aapi0018	Sequence		793	395.5	43.6	165	2	AAW43382	Aaw43382	Human	int
721	397.5	43.8	188	2	AAV42486	Aav42486	Human	int	794	395.5	43.6	165	8	ADL90580	Adl90580	Human	int
722	397.5	43.8	188	3	AAV69484	Aay69484	Human	int	795	395.5	43.6	165	8	ADL90548	Adl90548	Human	mut
723	397.5	43.8	188	5	AAE15828	Aae15828	Human	int	796	395.5	43.6	165	8	ADL90576	Adl90576	Human	mut
724	397.5	43.8	188	5	AAE18957	Aae18957	Human	alp	797	395.5	43.6	165	8	ADL90591	Adl90591	Human	mut
725	397.5	43.8	188	5	ABB07434	Abb07434	Interfero		798	395.5	43.6	165	8	ADL90521	Adl90521	Human	mut
726	397.5	43.8	188	6	ABR55840	Abrr55840	Human	int	799	395.5	43.6	165	8	ADL90579	Adl90579	Human	mut
727	397.5	43.8	188	6	AAO16454	Aao16454	Human	int	800	395.5	43.6	165	8	ADL90621	Adl90621	Human	mut
728	397.5	43.8	188	8	ADPF7247	Aadf7247	Interfero		801	395.5	43.6	165	8	ADL90634	Adl90634	Human	mut
729	397.5	43.8	188	8	ADL24486	Adl24486	Human	int	802	395.5	43.6	165	8	ADL90665	Adl90665	Human	mut
730	397.5	43.8	188	8	ADN49676	Adn49676	Human	int	803	395.5	43.6	165	8	ADL90654	Adl90654	Human	mut
731	397.5	43.8	198	5	AAE16138	Aae16138	Human	IFN	804	395.5	43.6	165	8	ADL90500	Adl90500	Human	mut
732	397.5	43.8	274	2	AAV02094	Aay02094	A multifu		805	395.5	43.6	165	8	ADL90607	Adl90607	Human	mut
733	397.5	43.8	274	2	AAV02098	Aay02098	A multifu		806	395.5	43.6	165	8	ADL90534	Adl90534	Human	mut
734	397.5	43.8	327	4	AAAB72223	Aab72223	Fusion pr		807	395.5	43.6	165	8	ADL90509	Adl90509	Human	mut
735	397.5	43.8	396	6	ADRA49580	Adra49580	Human	Igg	808	395.5	43.6	165	8	ADL90513	Adl90513	Human	mut
736	397.5	43.8	411	8	ADRA49602	Adra49602	Human	Igg	809	395.5	43.6	165	8	ADL90556	Adl90556	Human	mut
737	397.5	43.8	453	2	AAV02096	Aay02096	A multifu		810	395.5	43.6	165	8	ADL90578	Adl90578	Human	mut
738	397.5	43.8	769	7	ADPF15090	Aadf15090	Human	alb	811	395.5	43.6	165	8	ADL90590	Adl90590	Human	mut
739	397.5	43.8	769	7	ADPF15111	Aadf15111	Human	alb	812	395.5	43.6	165	8	ADL90587	Adl90587	Human	mut
740	397.5	43.8	769	7	ADH21331	Aadh21331	Human	alb	813	395.5	43.6	165	8	ADL88760	Adl88760	Human	mut
741	397.5	43.8	769	7	ADH21318	Aadh21318	Human	alb	814	395.5	43.6	165	8	ADL88679	Adl88679	Human	mod
742	397.5	43.8	773	7	ADPF15107	Aadf15107	Human	alb	815	395.5	43.6	165	8	ADL88704	Adl88704	Human	mod
743	397.5	43.8	773	7	ADH21328	Aadh21328	Human	alb	816	395.5	43.6	165	8	ADL88746	Adl88746	Human	mod
744	397.5	43.8	774	7	ADPF15106	Aadf15106	Human	alb	817	395.5	43.6	165	8	ADL88761	Adl88761	Human	mod
745	397.5	43.8	774	7	ADPF16213	Aadf16213	Human	alb	818	395.5	43.6	165	8	ADL88824	Adl88824	Human	mod
746	397.5	43.8	774	7	ADPF15056	Aadf15056	Human	alb	819	395.5	43.6	165	8	ADL88778	Adl88778	Human	mod
747	397.5	43.8	774	7	ADH21306	Aadh21306	Human	alb	820	395.5	43.6	165	8	ADL88777	Adl88777	Human	mod
748	397.5	43.8	774	7	ADH21655	Aadh21655	Human	alb	821	395.5	43.6	165	8	ADL88683	Adl88683	Human	mod
749	397.5	43.8	835	7	ADH21327	Aadh21327	Human	alb	822	395.5	43.6	165	8	ADL88726	Adl88726	Human	mod
750	397.5	43.8	835	7	ADPF15101	Aadf15101	Human	alb	823	395.5	43.6	165	8	ADL88757	Adl88757	Human	mod
751	397.5	43.8	835	7	ADH21323	Aadh21323	Human	alb	824	395.5	43.6	165	8	ADL88749	Adl88749	Human	mod
752	396.5	43.7	165	1	AAPE60221	Aape60221	Sequence		825	395.5	43.6	165	8	ADL88750	Adl88750	Human	mod
753	396.5	43.7	165	1	AAPE70327	Aape70327	Recombina		826	395.5	43.6	165	8	ADL88691	Adl88691	Human	mod
754	396.5	43.7	165	1	AAW43385	Aaw43385	Human	int	827	395.5	43.6	165	8	ADL88748	Adl88748	Human	mod
755	396.5	43.7	165	4	AAE06745	Aae06745	Human	int	828	395.5	43.6	165	8	ADL88835	Adl88835	Human	mod

829	395.5	43.6	165	8	ADL88670	Human	mod	902	393.5	43.4	165	8	ADL90651	ADL90651	Human	mut
830	395.5	43.6	165	8	ADL88791	Human	mod	903	393.5	43.4	165	8	ADL90600	ADL90600	Human	mut
831	395.5	43.6	165	8	ADL88804	Human	mod	904	393.5	43.4	165	8	ADL90695	ADL90695	Human	mut
832	395	43.6	166	8	AD032395	Human	IFN	905	393.5	43.4	165	8	ADL90698	ADL90698	Human	mut
833	395	43.6	216	2	AAAR3793	Natural	h	906	393.5	43.4	165	8	ADL90617	ADL90617	Human	mut
834	394.5	43.5	165	2	AAW43387	Human	int	907	393.5	43.4	165	8	ADL90650	ADL90650	Human	mut
835	394.5	43.5	165	3	AAAB01301	Wild type		908	393.5	43.4	165	8	ADL90677	ADL90677	Human	mut
836	394.5	43.5	165	4	AAAB4158	Human	int	909	393.5	43.4	165	8	ADL90649	ADL90649	Human	mut
837	394.5	43.5	165	4	ADL90516	Human	mut	910	393.5	43.4	165	8	ADL90538	ADL90538	Human	mut
838	394.5	43.5	165	8	ADL90555	Human	mut	911	393.5	43.4	165	8	ADL90610	ADL90610	Human	mut
839	394.5	43.5	165	8	ADL90518	Human	mut	912	393.5	43.4	165	8	ADL90616	ADL90616	Human	mut
840	394.5	43.5	165	8	ADL90594	Human	mut	913	393.5	43.4	165	8	ADL90619	ADL90619	Human	mut
841	394.5	43.5	165	8	ADL90630	Human	mut	914	393.5	43.4	165	8	ADL90648	ADL90648	Human	mut
842	394.5	43.5	165	8	ADL90585	Human	mut	915	393.5	43.4	165	8	ADL90632	ADL90632	Human	mut
843	394.5	43.5	165	8	ADL90541	Human	mut	916	393.5	43.4	165	8	ADL90536	ADL90536	Human	mut
844	394.5	43.5	165	8	ADL90532	Human	mut	917	393.5	43.4	165	8	ADL90676	ADL90676	Human	mut
845	394.5	43.5	165	8	ADL90592	Human	mut	918	393.5	43.4	165	8	ADL89646	ADL89646	Human	mut
846	394.5	43.5	165	8	ADL90530	Human	mut	919	393.5	43.4	165	8	ADL88770	ADL88770	Human	mut
847	394.5	43.5	165	8	ADL90572	Human	mut	920	393.5	43.4	165	8	ADL88787	ADL88787	Human	mut
848	394.5	43.5	165	8	ADL90631	Human	mut	921	393.5	43.4	165	8	ADL88780	ADL88780	Human	mut
849	394.5	43.5	165	8	ADL90608	Human	mut	922	393.5	43.4	165	8	ADL88820	ADL88820	Human	mut
850	394.5	43.5	165	8	ADL90515	Human	mut	923	393.5	43.4	165	8	ADL88821	ADL88821	Human	mut
851	394.5	43.5	165	8	ADL90583	Human	mut	924	393.5	43.4	165	8	ADL88802	ADL88802	Human	mut
852	394.5	43.5	165	8	ADL90550	Human	mut	925	393.5	43.4	165	8	ADL88786	ADL88786	Human	mut
853	394.5	43.5	165	8	ADL90562	Human	mut	926	393.5	43.4	165	8	ADL88789	ADL88789	Human	mut
854	394.5	43.5	165	8	ADL88778	Human	mod	927	393.5	43.4	165	8	ADL88819	ADL88819	Human	mod
855	394.5	43.5	165	8	ADL88702	Human	mod	928	393.5	43.4	165	8	ADL89649	ADL89649	Human	mod
856	394.5	43.5	165	8	ADL88848	Human	cyt	929	393.5	43.4	165	8	ADL88818	ADL88818	Human	mod
857	394.5	43.5	165	8	ADL88725	Human	mod	930	393.5	43.4	165	8	ADL88847	ADL88847	Human	mod
858	394.5	43.5	165	8	ADL88742	Human	mod	931	393.5	43.4	165	8	ADL88708	ADL88708	Human	mod
859	394.5	43.5	165	8	ADL88764	Human	mod	932	393.5	43.4	165	8	ADL88706	ADL88706	Human	mod
860	394.5	43.5	165	8	ADL89773	Human	cyt	933	393.5	43.4	165	8	ADL88846	ADL88846	Human	mod
861	394.5	43.5	165	8	ADL88688	Human	mod	934	393.5	43.4	187	1	AAAP20007	AAAP20007	Hybrid	hu
862	394.5	43.5	165	8	ADL88720	Human	mod	935	393	43.3	160	8	AD032408	AD032408	Human	IFN
863	394.5	43.5	165	8	ADL88801	Human	mod	936	393	43.3	166	1	AAAP60099	AAAP60099	Sequence	
864	394.5	43.5	165	8	ADL88762	Human	mod	937	393	43.3	166	1	AAAP90185	AAAP90185	Hybrid	al
865	394.5	43.5	165	8	ADL88800	Human	mod	938	393	43.3	166	8	AD032415	AD032415	Human	IFN
866	394.5	43.5	165	8	ADL88700	Human	mod	939	392.5	43.3	165	2	AAW43388	AAW43388	Human	int
867	394.5	43.5	165	8	ADL88711	Human	mod	940	392.5	43.3	165	8	ADL90609	ADL90609	Human	mut
868	394.5	43.5	165	8	ADL88686	Human	mod	941	392.5	43.3	165	8	ADL90613	ADL90613	Human	mut
869	394.5	43.5	165	8	ADL88685	Human	mod	942	392.5	43.3	165	8	ADL90573	ADL90573	Human	mut
870	394.5	43.5	165	8	ADL88753	Human	mod	943	392.5	43.3	165	8	ADL90675	ADL90675	Human	mut
871	394.5	43.5	165	8	ADL88755	Human	mod	944	392.5	43.3	165	8	ADL90547	ADL90547	Human	mut
872	394.5	43.5	165	8	ADL88732	Human	mod	945	392.5	43.3	165	8	ADL90554	ADL90554	Human	mut
873	394.5	43.5	165	8	ADN10801	Human	int	946	392.5	43.3	165	8	ADL90696	ADL90696	Human	mut
874	394.5	43.5	165	8	ADSL16311	Human	int	947	392.5	43.3	165	8	ADL90504	ADL90504	Human	mut
875	394.5	43.5	166	1	AAAP40022	Recombina		948	392.5	43.3	165	8	ADL90510	ADL90510	Human	mut
876	394.5	43.5	166	4	AAAB82337	Yeast-exp		949	392.5	43.3	165	8	ADL90512	ADL90512	Human	mut
877	394.5	43.5	175	1	AAAP30163	Sequence		950	392.5	43.3	165	8	ADL90586	ADL90586	Human	mut
878	394.5	43.5	182	2	AAAR05400	Hybrid	hu	951	392.5	43.3	165	8	ADL90545	ADL90545	Human	mut
879	394.5	43.5	188	1	AAAP20103	Sequence		952	392.5	43.3	165	8	ADL90582	ADL90582	Human	mut
880	394.5	43.5	188	4	AAAB31458	Amino aci		953	392.5	43.3	165	8	ADL90584	ADL90584	Human	mut
881	394.5	43.5	188	5	AAAE15826	Human	int	954	392.5	43.3	165	8	ADL90537	ADL90537	Human	mut
882	394.5	43.5	188	5	AAAB80767	Human	int	955	392.5	43.3	165	8	ADL90618	ADL90618	Human	mut
883	394.5	43.5	188	8	ADPF7281	Interfero		956	392.5	43.3	165	8	ADL90520	ADL90520	Human	mut
884	394.5	43.5	188	8	ADU99992	Human	IFN	957	392.5	43.3	165	8	ADL90567	ADL90567	Human	mut
885	394.5	43.5	188	8	ADMA1331	Human	int	958	392.5	43.3	165	8	ADL88743	ADL88743	Human	mod
886	394.5	43.5	188	8	ADN02798	Human	int	959	392.5	43.3	165	8	ADL88783	ADL88783	Human	mod
887	394.5	43.5	188	4	AAAB82338	Human	int	960	392.5	43.3	165	8	ADL88682	ADL88682	Human	mod
888	394.5	43.5	344	4	AAAB06343	Human	int	961	392.5	43.3	165	8	ADL88737	ADL88737	Human	mod
889	394	43.4	166	4	AAAG61809	Interfero		962	392.5	43.3	165	8	ADL88674	ADL88674	Human	mod
890	394	43.4	166	8	ADL29637	Human	int	963	392.5	43.3	165	8	ADL88717	ADL88717	Human	mod
891	394	43.4	166	8	AD032390	Human	IFN	964	392.5	43.3	165	8	ADL89647	ADL89647	Human	mod
892	394	43.4	166	8	AD032404	Human	IFN	965	392.5	43.3	165	8	ADL88707	ADL88707	Human	mod
893	394	43.4	166	8	AD032413	Human	IFN	966	392.5	43.3	165	8	ADL88754	ADL88754	Human	mod
894	394	43.4	166	8	AD032420	Human	IFN	967	392.5	43.3	165	8	ADL88756	ADL88756	Human	mod
895	394	43.4	166	8	AD032416	Human	IFN	968	392.5	43.3	165	8	ADL88845	ADL88845	Human	mod
896	394	43.4	166	8	AD032419	Human	IFN	969	392.5	43.3	165	8	ADL88690	ADL88690	Human	mod
897	394	43.4	166	8	AD032422	Human	IFN	970	392.5	43.3	165	8	ADL88779	ADL88779	Human	mod
898	394	43.4	166	8	AD032392	Human	IFN	971	392.5	43.3	165	8	ADL88788	ADL88788	Human	mod
899	394	43.4	189	5	ABG68064	Human	int	972	392.5	43.3	165	8	ADL88752	ADL88752	Human	mod
900	393.5	43.4	165	2	AAW43383	Human	int	973	392.5	43.3	165	8	ADL88680	ADL88680	Human	mod
901	393.5	43.4	165	7	ADL13053	Modified		974	392.5	43.3	165	8	ADL88715	ADL88715	Human	mod

975	392.5	43.3	165	8	ADL88724	Human mod	1048	389.5	42.9	165	8	ADL90629	ADL90629	Human mut
976	392	43.2	166	4	AA61822	Interfero	1049	389.5	42.9	165	8	ADL90544	ADL90544	Human mut
977	392	43.2	166	4	ADL29650	Human int	1050	389.5	42.9	165	8	ADL90639	ADL90639	Human mut
978	392	43.2	166	8	AD032399	Human IFN	1051	389.5	42.9	165	8	ADL90522	ADL90522	Human mut
979	392	43.2	166	8	AD032391	Human IFN	1052	389.5	42.9	165	8	ADL90543	ADL90543	Human mut
980	392	43.2	189	4	AA849782	Human alp	1053	389.5	42.9	165	8	ADL90552	ADL90552	Human mut
981	392	43.2	189	7	ADF94974	Human int	1054	389.5	42.9	165	8	ADL88814	ADL88814	Human mod
982	391.5	43.2	165	2	AAW43390	Human int	1055	389.5	42.9	165	8	ADL88784	ADL88784	Human mod
983	391.5	43.2	165	2	AAW43386	Human int	1056	389.5	42.9	165	8	ADL88713	ADL88713	Human mod
984	391.5	43.2	165	7	ADL13046	Wild-cype	1057	389.5	42.9	165	8	ADL88652	ADL88652	Human mod
985	391.5	43.2	165	8	ADL25136	Human int	1058	389.5	42.9	165	8	ADL88694	ADL88694	Human mod
986	391.5	43.2	165	8	ADL90561	Human mut	1059	389.5	42.9	165	8	ADL88828	ADL88828	Human mod
987	391.5	43.2	165	8	ADL90560	Human mut	1060	389.5	42.9	165	8	ADL88714	ADL88714	Human mod
988	391.5	43.2	165	8	ADL90611	Human mut	1061	389.5	42.9	165	8	ADL88722	ADL88722	Human mod
989	391.5	43.2	165	8	ADL90703	Human mut	1062	389.5	42.9	165	8	ADL88739	ADL88739	Human mod
990	391.5	43.2	165	8	ADL90566	Human mut	1063	389.5	42.9	165	8	ADL89650	ADL89650	Human mod
991	391.5	43.2	165	8	ADL90571	Human mut	1064	389.5	42.9	165	8	ADL88696	ADL88696	Human mod
992	391.5	43.2	165	8	ADL90667	Human mut	1065	389.5	42.9	165	8	ADL88843	ADL88843	Human mod
993	391.5	43.2	165	8	ADL90701	Human mut	1066	389.5	42.9	165	8	ADL88716	ADL88716	Human mod
994	391.5	43.2	165	8	ADL90525	Human mut	1067	389.5	42.9	165	8	ADL88705	ADL88705	Human mod
995	391.5	43.2	165	8	ADL90693	Human mut	1068	389.5	42.9	166	1	AAp40759	AAp40759	Human int
996	391.5	43.2	165	8	ADL90540	Human mut	1069	389.5	42.9	430	4	AA655234	AA655234	Human leu
997	391.5	43.2	165	8	ADL90507	Human mut	1070	389.5	42.9	166	8	AD032402	AD032402	Human IFN
998	391.5	43.2	165	8	ADL90527	Human mut	1071	388.5	42.8	165	8	ADL90645	ADL90645	Human mut
999	391.5	43.2	165	8	ADL90539	Human mut	1072	388.5	42.8	165	8	ADL90674	ADL90674	Human mut
1000	391.5	43.2	165	8	ADL90666	Human mut	1073	388.5	42.8	165	8	ADL90659	ADL90659	Human mut
1001	391.5	43.2	165	8	ADL90601	Human mut	1074	388.5	42.8	165	8	ADL90519	ADL90519	Human mut
1002	391.5	43.2	165	8	ADL90514	Human mut	1075	388.5	42.8	165	8	ADL90564	ADL90564	Human mut
1003	391.5	43.2	165	8	ADL90523	Human mut	1076	388.5	42.8	165	8	ADL90569	ADL90569	Human mut
1004	391.5	43.2	165	8	ADL88695	Human mod	1077	388.5	42.8	165	8	ADL88689	ADL88689	Human mod
1005	391.5	43.2	165	8	ADL88836	Human mod	1078	388.5	42.8	165	8	ADL88844	ADL88844	Human mod
1006	391.5	43.2	165	8	ADL88741	Human mod	1079	388.5	42.8	165	8	ADL88829	ADL88829	Human mod
1007	391.5	43.2	165	8	ADL88693	Human mod	1080	388.5	42.8	165	8	ADL88734	ADL88734	Human mod
1008	391.5	43.2	165	8	ADL88644	Human mod	1081	388.5	42.8	165	8	ADL88815	ADL88815	Human mod
1009	391.5	43.2	165	8	ADL88731	Human mod	1082	388.5	42.8	165	8	ADL88739	ADL88739	Human mod
1010	391.5	43.2	165	8	ADL88709	Human mod	1083	388.5	42.8	165	8	ADR49612	ADR49612	Human int
1011	391.5	43.2	165	8	ADL89652	Human mod	1084	388.5	42.8	336	8	ADR49590	ADR49590	Human Igg
1012	391.5	43.2	165	8	ADL88697	Human mod	1085	388.5	42.8	165	8	ADR49060	ADR49060	Human int
1013	391.5	43.2	165	8	ADL88736	Human mod	1086	388	42.8	189	6	AA015998	AA015998	Mutant hu
1014	391.5	43.2	165	8	ADL88730	Human mod	1087	387.5	42.7	165	8	ADL90656	ADL90656	Human mut
1015	391.5	43.2	165	8	ADL88781	Human mod	1088	387.5	42.7	165	8	ADL90642	ADL90642	Human mut
1016	391.5	43.2	165	8	ADL89654	Human mod	1089	387.5	42.7	165	8	ADL88826	ADL88826	Human mod
1017	391.5	43.2	165	8	ADL88684	Human mod	1090	387.5	42.7	165	8	ADL88812	ADL88812	Human mod
1018	391.5	43.2	165	8	ADL88710	Human mod	1091	387.5	42.7	164	1	AAp60119	AAp60119	Interfero
1019	391.5	43.2	165	8	ADL88771	Human mod	1092	387	42.7	167	3	AAV51930	AAV51930	Human alp
1020	391.5	43.2	165	8	ADL88677	Human mod	1093	386.5	42.6	165	5	AB668843	AB668843	Interfero
1021	391.5	43.2	166	2	AA838792	Recombina	1094	386.5	42.6	165	7	ADL13054	ADL13054	Modified
1022	391	43.1	166	8	AD032418	Human IFN	1095	386.5	42.6	165	8	ADL90640	ADL90640	Human mut
1023	391	43.1	166	8	AD032414	Human IFN	1096	386.5	42.6	165	8	ADL90652	ADL90652	Human mut
1024	391	43.1	166	8	AD032417	Human IFN	1097	386.5	42.6	165	8	ADL90641	ADL90641	Human mut
1025	391	43.1	166	8	AD032423	Human IFN	1098	386.5	42.6	165	8	ADL90636	ADL90636	Human mut
1026	391	43.1	166	8	AD032421	Human IFN	1099	386.5	42.6	165	8	ADL90657	ADL90657	Human mut
1027	391	43.1	189	1	AAp10017	Sequene	1100	386.5	42.6	165	8	ADL88822	ADL88822	Human mod
1028	390.5	43.1	165	2	AAW43389	Human int	1101	386.5	42.6	165	8	ADL88811	ADL88811	Human mod
1029	390.5	43.1	165	8	ADL25148	Human IFN	1102	386.5	42.6	165	8	ADL88827	ADL88827	Human mod
1030	390.5	43.1	165	8	ADL90660	Human mut	1103	386.5	42.6	165	8	ADL88806	ADL88806	Human mod
1031	390.5	43.1	165	8	ADL90638	Human mut	1104	386.5	42.6	165	8	ADL88810	ADL88810	Human mod
1032	390.5	43.1	165	8	ADL90639	Human mut	1105	386	42.6	166	1	AAp60036	AAp60036	Sequene
1033	390.5	43.1	165	8	ADL88808	Human mod	1106	386	42.6	166	2	AA842812	AA842812	Lymphobla
1034	390.5	43.1	165	8	ADL88809	Human mod	1107	386	42.6	166	5	AB668083	AB668083	Human int
1035	390.5	43.1	165	8	ADL88830	Human mod	1108	386	42.6	166	8	ADL88861	ADL88861	Human cyt
1036	390	43.0	166	8	AD032400	Human IFN	1109	386	42.6	166	8	AD032380	AD032380	Human int
1037	390	43.0	166	8	AD032401	Human IFN	1110	386	42.6	166	8	AD032406	AD032406	Human IFN
1038	390	43.0	166	8	AD032403	Human IFN	1111	386	42.6	166	8	AD032407	AD032407	Human IFN
1039	390	43.0	166	8	AD032394	Human IFN	1112	386	42.6	166	8	ADR23067	ADR23067	Human int
1040	389.5	42.9	165	8	ADL90658	Human mut	1113	386	42.6	167	1	AAp30186	AAp30186	Sequene
1041	389.5	42.9	165	8	ADL90644	Human mut	1114	386	42.6	167	1	AAp40130	AAp40130	Sequene
1042	389.5	42.9	165	8	ADL90535	Human mut	1115	386	42.6	189	1	AAp30183	AAp30183	Sequene
1043	389.5	42.9	165	8	ADL90673	Human mut	1116	386	42.6	189	1	AAp40741	AAp40741	Sequene
1044	389.5	42.9	165	8	ADL90526	Human mut	1117	386	42.6	189	1	AAp40127	AAp40127	Sequene
1045	389.5	42.9	165	8	ADL90546	Human mut	1118	386	42.6	189	2	AAW73231	AAW73231	Porcine i
1046	389.5	42.9	165	8	ADL90524	Human mut	1119	386	42.6	189	2	AAW83902	AAW83902	Porcine i
1047	389.5	42.9	165	8	ADL90614	Human mut	1120	386	42.6	189	5	ABG32987	ABG32987	Porcine i

1121	386	42.6	189	5	ABB80768	Abb80768	Human	int	1194	374.5	41.3	165	7	AD113050	Ad113050	Modified
1122	386	42.6	189	5	ABB07428	Abb07428	Interfero		1195	374.5	41.3	170	1	AAp60319	Aap60319	Sequence
1123	386	42.6	189	5	AAg78573	Aag78573	Human	int	1196	374	41.2	167	1	AAb49176	Aab49176	Mouse
1124	386	42.6	189	6	AAo15999	Aao15999	Mutant	hu	1197	373.5	41.2	150	5	ABG68840	Abg68840	Interfero
1125	385.5	42.5	165	8	ADL90661	Adl90661	Human	mut	1198	373.5	41.2	150	5	ABG68842	Abg68842	Interfero
1126	385.5	42.5	165	8	ADL90637	Adl90637	Human	mut	1199	373.5	41.2	150	5	ABG68841	Abg68841	Interfero
1127	385.5	42.5	165	8	ADL90653	Adl90653	Human	mut	1200	373.5	41.2	165	8	ADRA4609	Adra4609	Human
1128	385.5	42.5	165	8	ADL88823	Adl88823	Human	mod	1201	373.5	41.2	165	8	ADRA4608	Adra4608	Human
1129	385.5	42.5	165	8	ADL88831	Adl88831	Human	mod	1202	373.5	41.2	165	8	ADRA4595	Adra4595	Human
1130	385.5	42.5	165	8	ADL88807	Adl88807	Human	mod	1203	373.5	41.2	165	8	ADRA4598	Adra4598	Human
1131	385.5	42.5	165	8	ADL9613	Adl9613	Human	int	1204	372	41.0	133	1	AAp20109	Aap20109	Sequence
1132	385.5	42.5	219	2	AAr11356	Aar11356	Alkeline		1205	372	41.0	167	4	AAb49172	Aab49172	Mouse
1133	385.5	42.5	165	8	ADRA4589	Adra4589	Human	IGG	1206	371.5	41.0	395	8	ADRA4596	Adra4596	Human
1134	385	42.4	166	8	ADQ32405	Adq32405	Human	IFN	1207	371.5	41.0	396	8	ADRA4597	Adra4597	Human
1135	384.5	42.4	165	8	ADL90628	Adl90628	Human	mut	1208	371	40.9	396	1	AAp30074	Aap30074	Sequence
1136	384.5	42.4	165	8	ADL90635	Adl90635	Human	mut	1209	371	40.9	189	1	AAW73225	Aaw73225	Bovine
1137	384.5	42.4	165	8	ADL88798	Adl88798	Human	mod	1210	371	40.9	189	2	AAW83896	Aaw83896	Bovine
1138	384.5	42.4	165	8	ADL88805	Adl88805	Human	mod	1211	371	40.9	189	5	ABG32981	Abg32981	Bovine
1139	384.5	42.4	165	8	ADRA4582	Adra4582	Human	int	1212	370	40.8	99	2	AAW09285	Aaw09285	Human
1140	384.5	42.4	396	8	ADRA4582	Adra4582	Human	IGG	1213	370	40.8	99	2	AAW44112	Aaw44112	Human
1141	384	42.3	166	1	AAp60100	Aap60100	Sequence		1214	368.5	40.6	150	2	AAr11355	Aar11355	Interfero
1142	384	42.3	166	1	AAp90186	Aap90186	Hydrid	al	1215	368.5	40.6	165	5	ABG68844	Abg68844	Interfero
1143	383.5	42.3	165	8	ADL90551	Adl90551	Human	mut	1216	368	40.6	189	1	AAp50328	Aap50328	Bovine
1144	383.5	42.3	165	8	ADL90643	Adl90643	Human	mut	1217	367.5	40.5	156	8	ADSL6340	Adsl6340	Human
1145	383.5	42.3	165	8	ADL90570	Adl90570	Human	mut	1218	367.5	40.5	165	8	ADRA4606	Adra4606	Human
1146	383.5	42.3	165	8	ADL90646	Adl90646	Human	mut	1219	367.5	40.5	396	8	ADRA4600	Adra4600	Human
1147	383.5	42.3	165	8	ADL90697	Adl90697	Human	mut	1220	367.5	40.5	411	8	ADRA4601	Adra4601	Human
1148	383.5	42.3	165	8	ADL88816	Adl88816	Human	mod	1221	367	40.5	200	5	AAU77407	Aau77407	Human
1149	383.5	42.3	165	8	ADL88813	Adl88813	Human	mod	1222	366.5	40.4	155	8	ADSL6336	Adsl6336	Human
1150	383.5	42.3	165	8	ADL88740	Adl88740	Human	mod	1223	366.5	40.4	165	8	ADRA4603	Adra4603	Human
1151	383.5	42.3	165	8	ADL88721	Adl88721	Human	mod	1224	366.5	40.4	227	8	AAW47208	Aaw47208	Human
1152	383.5	42.3	165	8	ADL88648	Adl88648	Human	mod	1225	365.5	40.3	165	8	ADRA4605	Adra4605	Human
1153	383	42.2	166	4	AAb49174	Aab49174	Mouse	int	1226	364	40.1	97	2	AAW09283	Aaw09283	Human
1154	382.5	42.2	165	8	ADL90647	Adl90647	Human	mut	1227	364	40.1	97	2	AAW44115	Aaw44115	Human
1155	382.5	42.2	165	8	ADL88817	Adl88817	Human	mod	1228	363.5	40.1	165	5	ADRA4604	Adra4604	Human
1156	382	42.1	189	5	ABG68073	Abg68073	Human	int	1229	363.5	40.1	168	5	ABG68847	Abg68847	Interfero
1157	381.5	42.1	165	8	ADRA4610	Adra4610	Human	int	1230	363	40.0	166	5	ABG68042	Abg68042	Feline
1158	381.5	42.1	396	8	ADRA4594	Adra4594	Human	IGG	1231	363	40.0	166	5	ABG68042	Abg68042	Feline
1159	380.5	42.0	165	8	ADRA4607	Adra4607	Human	int	1232	362.5	40.0	155	8	ADSL6332	Adsl6332	Human
1160	380.5	42.0	396	8	ADRA4599	Adra4599	Human	IGG	1233	362.5	40.0	165	7	ADL13051	Adl13051	Modified
1161	380	41.9	167	4	AAb49178	Aab49178	Mouse	int	1234	360.5	39.7	165	7	ADL13052	Adl13052	Modified
1162	380	41.9	189	5	ABG68074	Abg68074	Human	int	1235	360	39.7	189	1	AAp50326	Aap50326	Bovine
1163	379.5	41.8	165	8	ADRA4611	Adra4611	Human	int	1236	359	39.6	166	4	AAE03047	Aae03047	Felis
1164	379.5	41.8	396	8	ADRA4592	Adra4592	Human	IGG	1237	359	39.6	189	4	AAE03046	Aae03046	Felis
1165	378.5	41.7	159	8	ADQ32410	Adq32410	Human	IFN	1238	358.5	39.5	151	8	ADSL6328	Adsl6328	Human
1166	378	41.7	166	4	AAb49161	Aab49161	Human	int	1239	358	39.5	166	3	AAy58828	Aay58828	Feline
1167	378	41.7	166	4	ADL88854	Adl88854	Human	cyt	1240	358	39.5	166	4	AAE03041	Aae03041	Felis
1168	378	41.7	166	8	ADQ32378	Adq32378	Human	int	1241	358	39.5	170	1	AAp20107	Aap20107	Sequence
1169	378	41.7	189	1	AAp30100	Aap30100	Sequence		1242	358	39.5	189	3	AAy58826	Aay58826	Feline
1170	378	41.7	189	5	ABB07430	Abb07430	Interfero		1243	358	39.5	189	4	AAE03039	Aae03039	Felis
1171	378	41.7	189	5	AAg78565	Aag78565	Human	int	1244	356	39.3	99	2	AAW09284	Aaw09284	Human
1172	378	41.7	189	6	AAO15996	Aao15996	Human	IFN	1245	356	39.3	166	3	AAy58827	Aay58827	Feline
1173	378	41.7	189	8	ADN10805	Adn10805	Human	int	1246	356	39.3	166	4	AAE03040	Aae03040	Felis
1174	378	41.7	189	8	ADSL6315	Adsl6315	Human	int	1247	356	39.3	166	4	AAE03043	Aae03043	Felis
1175	377.5	41.6	396	8	ADRA4591	Adra4591	Human	IGG	1248	356	39.3	174	8	ADL88850	Adl88850	Human
1176	377.5	41.6	396	8	ADRA4593	Adra4593	Human	IGG	1249	356	39.3	189	3	AAy58825	Aay58825	Feline
1177	377	41.6	161	1	AAp60305	Aap60305	Sequence		1250	356	39.3	189	4	AAE03038	Aae03038	Felis
1178	377	41.6	161	8	ADRA23068	Adra23068	Human	int	1251	356	39.3	189	1	AAE03042	Aae03042	Felis
1179	377	41.6	166	4	AAb49163	Aab49163	Human	int	1252	355	39.1	189	4	AAp50325	Aap50325	Sequence
1180	377	41.6	166	8	ADRA23066	Adra23066	Human	int	1253	353	38.9	189	1	AAp30075	Aap30075	Sequence
1181	377	41.6	189	1	AAp20104	Aap20104	Sequence		1254	353	38.9	189	2	AAW73226	Aaw73226	Bovine
1182	377	41.6	189	6	AAO16000	Aao16000	Mutant	hu	1255	353	38.9	189	2	AAW83897	Aaw83897	Bovine
1183	377	41.6	189	8	ADN10807	Adn10807	Human	int	1256	353	38.9	189	5	ABG32982	Abg32982	Pig
1184	377	41.6	189	8	ADSL6317	Adsl6317	Human	int	1257	352.5	38.9	170	4	AAb49785	Aab49785	Pig
1185	376	41.5	189	2	AAp30073	Aap30073	Sequence		1258	352.5	38.9	170	7	ADPFA977	Adpfa977	Pig
1186	376	41.5	189	2	AAW73224	Aaw73224	Bovine	in	1259	351	38.7	189	1	AAp50327	Aap50327	Bovine
1187	376	41.5	189	5	AAW83895	Aaw83895	Bovine	in	1260	349.5	38.5	171	4	AAE03045	Aae03045	Felis
1188	376	41.5	189	5	ABG32980	Abg32980	Bovine	le	1261	349.5	38.5	194	4	AAE03044	Aae03044	Felis
1189	375.5	41.4	473	1	AAp60797	Aap60797	Interfero		1262	346.5	38.2	171	5	ABG68053	Abg68053	Feline
1190	375	41.3	166	4	AAb49171	Aab49171	Mouse	int	1263	346.5	38.2	171	5	ABG68044	Abg68044	Feline
1191	375	41.3	189	2	AAy22637	Aay22637	Murine	int	1264	345	38.0	166	5	ABG68052	Abg68052	Feline
1192	375	41.3	189	6	AAO16001	Aao16001	Mutant	hu	1265	344.5	38.0	170	2	AAr10845	Aar10845	Feline
1193	374.5	41.3	165	3	AAb01302	Abb01302	Altered	h	1266	344.5	38.0	171	5	ABG68048	Abg68048	Feline

1267	344.5	38.0	171	5	ABG68051	Abg68051	Feline	in	1340	289	31.9	208	3	AAy91981	AAy91981	Variant	h
1268	342	37.7	166	4	AAB49175	Aab49175	Mouse	int	1341	289	31.9	208	3	AAy92041	AAy92041	Variant	h
1269	340.5	37.5	170	4	AAG5045	Aag5045	Feline	pr	1342	289	31.9	208	5	AAE16805	AAE16805	Human	int
1270	340.5	37.5	170	5	AAE21798	Aae21798	Feline	om	1343	289	31.9	208	5	AAE16808	AAE16808	Human	int
1271	340.5	37.5	171	1	AAp90398	Aap90398	Feline	in	1344	287.5	31.7	184	4	AAp50281	AAp50281	Protein	s
1272	340.5	37.5	171	1	ABG68041	Abg68041	Feline	in	1345	287.5	31.7	164	4	AAAB49787	AAAB49787	Bovine	in
1273	340.5	37.5	171	5	ABG68045	Abg68045	Feline	in	1346	287.5	31.7	166	7	ADFP94979	ADFP94979	Bovine	in
1274	340.5	37.5	171	5	ABG68046	Abg68046	Feline	in	1347	287	31.6	208	3	AAy91985	AAy91985	Variant	h
1275	340.5	37.5	171	5	ABG68047	Abg68047	Feline	in	1348	287	31.6	208	5	AAE16807	AAE16807	Human	int
1276	340.5	37.5	194	1	AAp90399	Aap90399	Feline	in	1349	285	31.4	161	1	AAp80055	AAp80055	Sequence	
1277	340.5	37.5	194	7	ADE15965	Ade15965	Cat	inter	1350	282.5	31.1	165	1	AAp50280	AAp50280	Protein	s
1278	340.5	37.5	194	7	ADE15966	Ade15966	Cat	inter	1351	282.5	31.1	186	1	AAp30078	AAp30078	Sequence	
1279	340	37.5	166	4	AAAB49177	Aab49177	Mouse	int	1352	282.5	31.1	186	2	AAAP3229	AAAP3229	Bovine	in
1280	335	36.9	167	1	AAp30223	Aap30223	Sequence		1353	282.5	31.1	186	5	AAAB63900	AAAB63900	Bovine	in
1281	335	36.9	167	1	AAp60689	Aap60689	Hybrid	pr	1354	282.5	31.1	186	5	ABG32985	ABG32985	Bovine	le
1282	334.5	36.9	170	2	AAW58568	Aaw58568	Amino	aci	1355	280	30.9	193	3	AAy91979	AAy91979	Truncated	
1283	334.5	36.9	170	2	AAy07474	Aay07474	Recombina		1356	280	30.9	193	3	AAy91977	AAy91977	Variant	h
1284	333.5	36.8	171	5	ABG68043	Abg68043	Feline	in	1357	280	30.9	193	5	AAE16801	AAE16801	Human	int
1285	333.5	36.8	171	5	ABG68050	Abg68050	Feline	in	1358	280	30.9	193	5	AAE16799	AAE16799	Human	int
1286	333	36.7	167	7	ADFI17016	Adfi17016	Human	alb	1359	280	30.9	193	6	ABU62228	ABU62228	Human	int
1287	333	36.7	167	7	ADH22026	Adh22026	Human	IFN	1360	277	30.5	193	6	ABU62231	ABU62231	Human	int
1288	332.5	36.7	172	5	ABBO7441	Abbo7441	Interfero		1361	277	30.5	161	2	AAy25092	AAy25092	Synthetic	
1289	332	36.6	95	2	AAW09286	Aaw09286	Human	mat	1362	277	30.5	161	6	AAO30310	AAO30310	Human	int
1290	332	36.6	95	2	AAW44113	Aaw44113	Human	int	1363	277	30.5	192	3	AAy91978	AAy91978	Truncated	
1291	331.5	36.5	162	4	AAB49173	Aab49173	Mouse	int	1364	277	30.5	192	5	AAE16800	AAE16800	Human	int
1292	331.5	36.5	166	1	AAp80050	Aap80050	Sequence		1365	275.5	30.4	192	6	ABU62229	ABU62229	Human	int
1293	330.5	36.4	166	1	AAp30222	Aap30222	Sequence		1366	275.5	30.4	192	6	ABU62229	ABU62229	Human	int
1294	330.5	36.4	166	1	AAp60688	Aap60688	Hybrid	pr	1367	273	30.1	166	1	AAp50025	AAp50025	Sequence	
1295	330.5	36.4	166	7	ADFI17017	Adfi17017	Human	alb	1368	272.5	30.0	166	1	AAp50030	AAp50030	Sequence	
1296	330.5	36.4	166	7	ADH22027	Adh22027	Human	IFN	1369	270.5	29.8	166	1	AAp50274	AAp50274	Protein	s
1297	329	36.3	167	1	AAp80051	Aap80051	Sequence		1370	270.5	29.8	166	1	AAp50028	AAp50028	Sequence	
1298	321	35.4	165	1	AAp50273	Aap50273	Protein	s	1371	270.5	29.8	1332	1	AAp70169	AAp70169	Sequence	
1299	319	35.2	157	5	ABG68060	Abg68060	Human	int	1372	269.5	29.7	166	1	AAp50029	AAp50029	Sequence	
1300	318	35.1	166	1	AAp50270	Aap50270	Protein	s	1373	268.5	29.6	166	1	AAp50031	AAp50031	Sequence	
1301	316	34.8	187	1	AAp60401	Aap60401	Canine	IF	1374	267.5	29.5	166	1	AAp50032	AAp50032	Sequence	
1302	316	34.8	187	1	AAp60402	Aap60402	Canine	IF	1375	265.5	29.3	166	1	AAp50024	AAp50024	Sequence	
1303	313	34.5	166	1	AAp50275	Aap50275	Protein	s	1376	264.5	29.2	165	1	AAp50207	AAp50207	Modified	
1304	312	34.4	132	6	ABU52320	Abu52320	Human	GPC	1377	264.5	29.2	166	1	AAp50194	AAp50194	Modified	
1305	312	34.4	132	6	ADL23975	Adl23975	Human	NOV	1378	264.5	29.2	166	1	AAp50196	AAp50196	Modified	
1306	312	34.4	151	6	ABU52319	Abu52319	Human	GPC	1379	264.5	29.2	166	1	AAp50023	AAp50023	Sequence	
1307	312	34.4	151	6	ADL23973	Adl23973	Human	NOV	1380	264	29.1	90	3	AAy55967	AAy55967	Partial	h
1308	311	34.3	166	4	AAG61825	Aag61825	Interfero		1381	263.5	29.1	166	1	AAp50272	AAp50272	Protein	s
1309	311	34.3	166	8	ADL29653	Adl29653	Human	int	1382	263.5	29.1	166	1	AAp50206	AAp50206	Modified	
1310	308	34.0	166	1	AAp50276	Aap50276	Protein	s	1383	263.5	29.1	166	1	AAp50193	AAp50193	Modified	
1311	307	33.8	165	1	AAp30227	Aap30227	Sequence		1384	263.5	29.1	166	1	AAp50027	AAp50027	Sequence	
1312	302	33.3	155	8	ADSL6329	Adsl6329	Human	int	1385	263.5	29.1	166	8	ADL90875	ADL90875	Human	mut
1313	301	33.2	156	8	ADSL6341	Adsl6341	Human	int	1386	263.5	29.1	166	8	ADL90985	ADL90985	Human	mut
1314	300	33.1	155	8	ADSL6337	Adsl6337	Human	int	1387	263.5	29.1	166	8	ADL98949	ADL98949	Human	mod
1315	296	32.6	155	8	ADSL6333	Adsl6333	Human	int	1388	263.5	29.1	166	8	ADL98959	ADL98959	Human	mod
1316	294	32.4	208	3	AAy91986	AAy91986	Human	int	1389	262	28.9	180	8	ADN10826	ADN10826	Human	int
1317	294	32.4	208	3	AAy91982	AAy91982	Variant	h	1390	261.5	28.8	166	8	ADL90748	ADL90748	Human	mut
1318	294	32.4	208	5	AAE16796	Aae16796	Human	int	1391	261.5	28.8	166	8	ADL89722	ADL89722	Human	mod
1319	294	32.4	208	5	AAAG78563	Aag78563	Human	int	1392	261	28.7	180	8	ADN10825	ADN10825	Human	int
1320	294	32.4	208	6	ABU62225	Abu62225	Human	int	1393	260.5	28.7	166	1	AAp50271	AAp50271	Protein	s
1321	293	32.3	120	5	ABBO4303	Abbo4303	Recombina		1394	260.5	28.6	166	1	ADL88992	ADL88992	Human	mod
1322	293	32.3	120	8	ADQ087760	Adq087760	Super-com		1395	259.5	28.6	166	1	AAp50278	AAp50278	Human	mod
1323	292	32.2	166	1	AAp50277	Aap50277	Protein	s	1396	259.5	28.6	166	8	ADL90862	ADL90862	Human	mut
1324	292	32.1	208	3	AAy91983	AAy91983	Variant	h	1397	259.5	28.6	166	8	ADL90876	ADL90876	Human	mut
1325	291	32.1	208	5	AAE16806	Aae16806	Human	int	1398	259.5	28.6	166	8	ADL98950	ADL98950	Human	mod
1326	290	32.0	161	1	AAp60691	Aap60691	Hybrid	pr	1399	259.5	28.6	166	4	ADL89836	ADL89836	Human	mod
1327	290	32.0	208	1	AAy06311	Aay06311	Human	int	1400	259	28.6	166	4	AAAB49371	AAAB49371	Human	INF
1328	290	32.0	208	3	AAy71466	AAy71466	Human	PRO	1401	258.5	28.5	166	1	AAp50032	AAp50032	Sequence	
1329	290	32.0	208	3	AAy91984	AAy91984	Variant	h	1402	258.5	28.5	166	1	AAp80047	AAp80047	Sequence	
1330	290	32.0	208	3	AAy91980	AAy91980	Human	int	1403	258.5	28.5	166	8	ADL90749	ADL90749	Human	mut
1331	290	32.0	208	5	AAE16795	Aae16795	Human	int	1404	258.5	28.5	166	8	ADL90915	ADL90915	Human	mut
1332	290	32.0	208	5	ABBO7424	Abbo7424	Interfero		1405	258.5	28.5	166	8	ADL90895	ADL90895	Human	mut
1333	290	32.0	208	5	ABBO7426	Abbo7426	Interfero		1406	258.5	28.5	166	8	ADL89723	ADL89723	Human	mod
1334	290	32.0	208	5	AAAG78562	Aag78562	Human	int	1407	258.5	28.5	166	8	ADL89869	ADL89869	Human	mod
1335	290	32.0	208	6	ABU62224	Abu62224	Human	int	1408	258.5	28.5	166	6	ADL89889	ADL89889	Human	mod
1336	290	32.0	208	6	ADCT8887	Adct8887	Human	PRO	1409	257.5	28.4	199	6	ABU09811	ABU09811	Human	int
1337	290	32.0	208	8	ADN10816	Adn10816	Human	int	1410	257.5	28.4	166	4	AAAB49378	AAAB49378	Human	INF
1338	290	32.0	208	8	ADSL6326	Adsl6326	Human	int	1411	257.5	28.4	166	4	AAU00130	AAU00130	Human	int
1339	290	32.0	215	7	ADML3725	Adml3725	Human	int	1412	257.5	28.4	166	4	AAU00112	AAU00112	Human	int

1413	257.5	28.4	166	4	AAU00149	AAU00149 Human int
1414	257.5	28.4	166	4	AAU00153	AAU00153 Human int
1415	257.5	28.4	166	4	AAU00156	AAU00156 Human int
1416	257.5	28.4	166	4	AAU00135	AAU00135 Human int
1417	257.5	28.4	166	6	ABR40020	ABR40020 Mutant in
1418	257.5	28.4	166	8	ADJ56141	ADJ56141 Human int
1419	257.5	28.4	166	8	ADL90734	ADL90734 Human mut
1420	257.5	28.4	166	8	ADL90758	ADL90758 Human mut
1421	257.5	28.4	166	8	ADL90882	ADL90882 Human mut
1422	257.5	28.4	166	8	ADL97877	ADL97877 Human IFN
1423	257.5	28.4	166	8	ADL89708	ADL89708 Human mod
1424	257.5	28.4	166	8	ADL89856	ADL89856 Human mod
1425	257.5	28.4	166	8	ADL88921	ADL88921 Human mod
1426	257.5	28.4	166	8	ADL88914	ADL88914 Human mod
1427	257.5	28.4	166	8	ADL89668	ADL89668 Human mod
1428	257.5	28.4	166	8	ADL89732	ADL89732 Human mod
1429	257.5	28.4	166	8	ADN10820	ADN10820 Human int
1430	257	28.3	166	4	AA849369	AA849369 Human INF
1431	257	28.3	166	8	ADL90852	ADL90852 Human mut
1432	257	28.3	166	8	ADL89826	ADL89826 Human mut
1433	257	28.3	166	1	AA60398	AA60398 Equine IF
1434	257	28.3	186	5	AAE29000	AAE29000 Equine in
1435	257	28.3	186	5	AAE29001	AAE29001 Porcine i
1436	256.5	28.3	165	8	ADL90735	ADL90735 Human mut
1437	256.5	28.3	165	8	ADL89709	ADL89709 Human mod
1438	256.5	28.3	166	1	AA850026	AA850026 Sequence
1439	256.5	28.3	166	2	AAW06574	AAW06574 Human int
1440	256.5	28.3	166	2	AAW47192	AAW47192 Interfero
1441	256.5	28.3	166	4	AAU00085	AAU00085 Human int
1442	256.5	28.3	166	4	AAU00071	AAU00071 Human int
1443	256.5	28.3	166	4	AAU00157	AAU00157 Human int
1444	256.5	28.3	166	4	AAU00086	AAU00086 Human int
1445	256.5	28.3	166	6	ABP72809	ABP72809 Human mat
1446	256.5	28.3	166	8	ADL90779	ADL90779 Human mut
1447	256.5	28.3	166	8	ADL90877	ADL90877 Human mut
1448	256.5	28.3	166	8	ADL88949	ADL88949 Human mod
1449	256.5	28.3	166	8	ADL89753	ADL89753 Human mod
1450	256.5	28.3	166	8	ADL88851	ADL88851 Human mod
1451	256.5	28.3	166	8	ADL88666	ADL88666 Human mod
1452	256.5	28.3	166	8	ADL88903	ADL88903 Human mod
1453	256.5	28.3	369	5	AAU99389	AAU99389 Mutant hu
1454	256	28.2	166	4	AA849370	AA849370 Human INF
1455	256	28.2	166	8	ADL90832	ADL90832 Human mut
1456	256	28.2	166	8	ADL90833	ADL90833 Human mut
1457	256	28.2	166	8	ADL90823	ADL90823 Human mut
1458	256	28.2	166	8	ADL89806	ADL89806 Human mod
1459	256	28.2	166	8	ADL89797	ADL89797 Human mod
1460	255	28.2	166	8	ADL89807	ADL89807 Human mod
1461	255.5	28.2	166	4	AAU00080	AAU00080 Human int
1462	255.5	28.2	166	4	AAU00114	AAU00114 Human int
1463	255.5	28.2	166	4	AAU00082	AAU00082 Human int
1464	255.5	28.2	166	6	ABP72808	ABP72808 Human mat
1465	255.5	28.2	166	8	ADL90743	ADL90743 Human mut
1466	255.5	28.2	166	8	ADL90912	ADL90912 Human mut
1467	255.5	28.2	166	8	ADL90767	ADL90767 Human mut
1468	255.5	28.2	166	8	ADL90746	ADL90746 Human mut
1469	255.5	28.2	166	8	ADL90878	ADL90878 Human mut
1470	255.5	28.2	166	8	ADL90782	ADL90782 Human mut
1471	255.5	28.2	166	8	ADL90851	ADL90851 Human mut
1472	255.5	28.2	166	8	ADL88912	ADL88912 Human mod
1473	255.5	28.2	166	8	ADL88911	ADL88911 Human mod
1474	255.5	28.2	166	8	ADL88720	ADL88720 Human mod
1475	255.5	28.2	166	8	ADL89717	ADL89717 Human mod
1476	255.5	28.2	166	8	ADL89741	ADL89741 Human mod
1477	255.5	28.2	166	8	ADL89852	ADL89852 Human mod
1478	255.5	28.2	166	8	ADL89886	ADL89886 Human mod
1479	255.5	28.2	166	8	ADL88906	ADL88906 Human mod
1480	255.5	28.2	166	8	ADL88913	ADL88913 Human mod
1481	255.5	28.2	166	8	ADL88950	ADL88950 Human mod
1482	255.5	28.2	166	8	ADL89756	ADL89756 Human mod
1483	255.5	28.2	166	8	ADL89825	ADL89825 Human mod
1484	255.5	28.2	423	3	AAV70869	AAV70869 Human int
1485	255.5	28.2	423	8	ADJ50907	ADJ50907 VCMV eigm

1486	255.5	28.2	423	8	AD043936	Ad043936 Amino aci
1487	255	28.1	166	4	AA849368	AA849368 Human INF
1488	255	28.1	166	8	ADL90828	AdL90828 Human mut
1489	255	28.1	166	8	ADL90835	AdL90835 Human mut
1490	255	28.1	166	8	ADL90867	AdL90867 Human mut
1491	255	28.1	166	8	ADL89802	AdL89802 Human mod
1492	255	28.1	166	8	ADL89809	AdL89809 Human mod
1493	255	28.1	166	8	ADL89841	AdL89841 Human mod
1494	255	28.1	180	8	ADN10829	Adn10829 Human int
1495	255	28.1	186	1	AA830079	AA830079 Sequence
1496	255	28.1	186	2	AAW73230	AAw73230 Bovine in
1497	255	28.1	186	2	AAW83901	AAw83901 Bovine in
1498	255	28.1	186	5	ABG32986	ABg32986 Bovine le
1499	255	28.1	775	7	ADL14951	ADl14951 Human alb
1500	255	28.1	775	7	ADH21287	Adh21287 Human alb

ALIGNMENTS

RESULT 1	
AA854768	
ID	AA854768 standard; protein; 172 AA.
XX	
AC	AA854768;
XX	
DT	25-MAR-2003 (revised)
DT	01-DEC-1994 (first entry)
XX	
DE	Sheep interferon-tau mature protein.
XX	
KW	Sheep; interferon-tau; immunostimulant; antitumor; virucide.
OS	Ovis aries.
XX	
PN	MO9410313-A2.
PD	11-MAY-1994.
XX	
PF	19-OCT-1993; 93MO-US010016.
XX	
PR	30-OCT-1992; 92US-00969890.
XX	
PA	(UYFL) UNIV FLORIDA.
PA	(WOME-) WOMEN'S RES INST.
XX	
PI	Bazer FW, Johnson HM, Pontzer CH, Ott TL, Van Heeke G, Imakawa K;
DR	WPI; 1994-167468/20.
XX	
PT	Interferon tau compens - lacking cytotoxic side effects when used as
XX	antivirals, and anti:cellular proliferation agents.
PS	Claim 3; Page 90; 126pp; English.
XX	
CC	This sheep IFN-tau protein is expressed in yeast, insect cells or E. coli
CC	using expression vector phage lambda-gu11. The protein is useful for
CC	inhibiting tumor cell growth, for inhibiting viral replication in cells
CC	and enhancing fertility in female mammals. (Updated on 25-MAR-2003 to
XX	correct PN field.)
SQ	Sequence 172 AA;

Query Match	100.0%;	Score 907;	DB 2;	Length 172;
Best Local Similarity	100.0%;	Pred. No. 1e-92;		
Matches 172;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	CYLSRKIMLDAREVKKILDMNRRLSPSCIQDKDFGLPEQWVWGDDLOKQDAFPVLYEM	60
Db	1	CYLSRKIMLDAREVKKILDMNRRLSPSCIQDKDFGLPEQWVWGDDLOKQDAFPVLYEM	60

Qy	61	LQSPFNLFYTHSSAAMDITLLLEQLCTGLQOQDLHDITCKGQVMGEEDSELGNNDPIVTV	120
----	----	--	-----

Db 61 LQOSFNLFTYEHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVWGEEDSELGNNDPIVTV 120
 QY 121 KKVFQGIYDYLOEKGYSDCAMEIVRVMRALTVSTTLQKRLTMGGDLNSP 172
 Db 121 KKVFQGIYDYLOEKGYSDCAMEIVRVMRALTVSTTLQKRLTMGGDLNSP 172

RESULT 2

AAR9397
 ID AAR9397 standard; procein; 172 AA.

AC AAR9397;

DT 29-DEC-1996 (first entry)

DE Ovine tau interferon (synthetic).

XX Tau interferon; ovine; bovine; autoimmune disease;

KM proliferative disorder; viral disease; fertility.

XX Synthetic.

XX WO9628183-A1.

XX 19-SEP-1996.

PF 15-MAR-1996; 96WO-US003472.

PR 16-MAR-1995; 95US-00406190.

XX (UYFL) UNIV FLORIDA.

PI Soos JM, Schiffendauer J, Johnson HM;

XX WPI; 1996-464609/46.

DR N-PSDB; AAT41504.

XX Tau interferon-concg. medicament - useful to treat autoimmune diseases,

PT proliferative disorder, viral diseases or to enhance fertility in a

XX female mammal.

XX Claim 5; Page 48; 65pp; English.

CC Ovine and human tau interferon may be used in medicaments to treat

CC autoimmune disorders (e.g. multiple sclerosis or rheumatoid arthritis), a

CC proliferative disorder (e.g. cancer) or a viral disease (e.g. hepatitis

CC B). It can also be used to enhance fertility in female mammals. The

CC medicament is given orally or by injection. Ovine and human tau

CC interferon sequences are given in AAT41504 to AAT41506

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XX AAW31698;

DT 14-APR-1998 (first entry)

DE Mature ovine interferon-tau (OvIFNtau) protein.

XX Interferon-tau; ovine; human; autoimmune disease; treatment; toxicity;

KM IFN tau; multiple sclerosis; diabetes mellitus; asthma; allergy; cancer.

XX Ovis aries.

XX WO9733607-A1.

XX 18-SEP-1997.

PF 12-MAR-1997; 97WO-US003794.

PR 15-MAR-1996; 96US-00616904.

XX (UYFL) UNIV FLORIDA.

PI Soos JM, Schiffendauer J, Johnson HM;

XX WPI; 1997-470642/43.

DR N-PSDB; AAV02288.

PT Oral administration of interferon-tau for treatment of auto-immune

PT disease - avoids toxicity of interferon alpha and generates fewer

XX specific antibodies than injection.

XX Claim 5; Page 31; 48pp; English.

CC This is a mature ovine interferon-tau (OvIFNtau) protein. The ovine and

CC the human interferon-tau (IFN tau) can be used in the treatment of

CC mammalian diseases responsive to IFN tau. The new feature in the

CC treatment is that IFN tau is administered orally. The method is used to

CC treat immune, particularly autoimmune disease, specifically multiple

CC sclerosis (a preferred application, reducing both severity and frequency

CC of relapses), type I diabetes mellitus, lupus erythematosus, amyotrophic

CC lateral sclerosis, Crohn's disease, rheumatoid arthritis, stomatitis,

CC asthma, allergies and psoriasis, particularly in humans or dogs. IFN tau

CC is also useful for treating cancer (e.g. hairy cell leukaemia, Kaposi's

CC sarcoma and multiple myeloma), cell proliferation and viral diseases

CC (hepatitis, human immunodeficiency virus etc., including prevention of

CC maternal transmission). It is also used for increasing fertility in

CC female mammals (increasing life time of the corpus luteum). Oral

CC administration is as effective as injection but is more convenient and

CC generates a lower level of anti-IFN tau antibodies. Use of IFN tau avoids

CC the toxicity associated with use of IFN alpha

XX

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RESULT 4

AAW44110
 ID AAW44110 standard; procein; 172 AA.

XX

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XX AAM44110;
 AC 16-JUN-1998 (first entry)
 XX
 XX
 XX
 XX Mature ovine interferon tau.
 DE
 XX Hybrid fusion; interferon-tau; inhibits tumour; viral growth; IFN-
 KM autolimmune disease; immune response.
 XX
 XX Ovis aries.
 OS
 XX MO9739127-A1.
 PN
 XX 23-OCT-1997.
 PD
 XX 11-APR-1997; 97WO-US006114.
 PF
 XX 12-APR-1996; 96US-0061328.
 PR
 XX (UYFL) UNIV FLORIDA.
 PA
 XX Johnson HM, Subramaniam PS, Pontzer CH;
 PI MPI; 1997-526463/48.
 XX N-PSDB; AAV02178.
 DR
 XX
 XX
 XX Hybrid nucleic acid encodes fusion of interferon-tau and other interferon
 PT - used to inhibit tumour and viral growth, and for treating auto-immune
 PT disease, less toxic than native type I interferon.
 XX
 XX Disclousure; Page 83; 147pp; English.
 PS
 XX The present sequence represents mature ovine interferon tau from the
 CC present invention. The present invention describes a novel chimeric
 CC nucleic acid which comprises: (i) a 5'-segment encoding the N-terminal
 CC amino acid (aa) sequence of an interferon tau (IFN τ) polypeptide; and
 CC (ii) a 3'-sequence encoding the C-terminal aa sequence of a non-tau type
 CC I interferon, with the two segments spliced in a region comprising part
 CC of the mature interferon between residues 8 and 37. Hybrid interferon
 CC fusion polypeptides are used to inhibit tumour growth (e.g. of steroid-
 CC sensitive tumours) and viral replication (e.g. of human immunodeficiency
 CC virus, hepatitis B or C virus, feline leukaemia virus) and to treat
 CC autoimmune diseases (e.g. lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis). Some hybrid interferon fusion polypeptides may
 CC block the antiviral/antiproliferative actions of IFN τ , so can be used to
 CC prevent immune responses induced by interferons, e.g. in organ
 CC transplantation. The hybrid interferon fusion polypeptides can also be
 CC used to raise antibodies, used e.g. for analysis of structure/function
 CC relationships. The novel chimeric nucleic acid is used to produce
 CC recombinant hybrid interferon fusion polypeptides. Hybrid interferon
 CC fusion polypeptides are less toxic than type I interferons, so can be
 CC administered at higher doses
 CC
 XX
 XX Sequence 172 AA;
 SQ
 Query Match 100.0%; Score 907; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1e-92;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 ABB07588
 ID ABB07588 standard; protein; 172 AA.
 XX
 XX
 XX ABB07588;
 AC
 XX 08-MAY-2002 (first entry)
 DT
 XX
 XX Ovine interferon-tau protein.
 DE
 XX Hepatitis C virus; HCV infection; ovine; interferon-tau; ovIFN-tau; OAS;
 KM 2',5'-oligoadenylate synthetase; virucide; hepatotropic; IFN-tau.
 XX
 XX Ovis aries.
 OS
 XX MO200206343-A2.
 PN
 XX 24-JAN-2002.
 PD
 XX 19-JUL-2001; 2001WO-US022976.
 PF
 XX 19-JUL-2000; 2000US-0219128P.
 PR 17-OCT-2000; 2000JP-00317160.
 XX
 XX (PEPG-) PEPGEN CORP.
 PA
 XX
 XX Sokawa Y, Liu C;
 PI MPI; 2002-179784/23.
 XX N-PSDB; ABA94936.
 DR
 XX
 XX
 XX Oral-delivery composition for treating conditions relating to hepatitis
 PT caused by hepatitis C virus, comprises ovine interferon-tau which
 PT stimulates bloodstream levels of 2',5'-oligoadenylate synthetase.
 XX
 XX Example 1; Page 32-33; 33pp; English.
 PS
 XX The invention provides an oral-delivery composition for use in treating
 CC hepatitis C virus (HCV) in a HCV-infected patient. The composition
 CC comprises ovine interferon-tau (ovIFN-tau), in a dosage effective to
 CC stimulate bloodstream levels of 2',5'-oligoadenylate synthetase (OAS).
 CC The ovIFN-tau synthesizes OAS which degrades viral mRNA. A method is also
 CC provided for monitoring the treatment of HCV by oral administration of
 CC ovIFN-tau, by measuring the blood levels of OAS prior to and after such
 CC oral administration, and if necessary, adjusting the dose of IFN-tau
 CC until a measurable increase in blood OAS level, relative to the level
 CC observed prior to administration. The composition is useful for treating
 CC hepatitis caused by HCV and the method is useful for monitoring treatment
 CC of HCV by oral administration of ovIFN-tau. The present sequence
 CC represents an ovine interferon-tau protein
 CC
 XX
 XX Sequence 172 AA;
 SQ
 Query Match 100.0%; Score 907; DB 5; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1e-92;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

XX AC AD117857;
XX XX
XX 22-APR-2004 (first entry)
XX DE Mature ovine interferon-tau, SEQ ID NO:2.
XX KM Interferon-tau; oral dosage form; oral administration; fasted state;
XX KM 2',5'-oligoadenylate synthetase; OAS; autoimmune condition;
XX KM multiple sclerosis; diabetes mellitus; Hashimoto's thyroiditis;
XX KM rheumatoid arthritis; uveitis; psoriasis; systemic lupus erythematosus;
XX KM allergy; asthma; eczema; Crohn's disease; ulcerative colitis;
XX KM viral infection; HIV infection; hepatitis;
XX KM cellular proliferation disorder; multiple myeloma; ovarian cancer;
XX KM hairy cell leukemia; inflammatory disease; immunosuppressive; virucide;
XX KM cytoskeletal; antiinflammatory; neuroprotective; antidiabetic;
XX KM thymostimetic; antirheumatic; antiarthritic; ophthalmological;
XX KM antiparasitic; dermatological; antiallergic; antiasthmatic; antilulcer;
XX KM anti-HIV; hepatotropic; vaccine; ovine; sheep.
XX OS Ovis aries.
XX OS Synthetic.
XX PN WO2003061728-A2.
XX PD 31-JUL-2003.
XX PF 16-JAN-2003; 2003WO-US001596.
XX PR 16-JAN-2002; 2002US-0349658P.
XX PA (PEPG-) PEPGEN CORP.
XX PI Sokawa Y, Liu C;
XX DR WPI; 2003-598711/56.
XX DR N-PSDB; AD117856.
XX PT An oral dosage form of interferon-tau administered to a subject in a
XX PT fasted state to achieve an increased level of 2',5'-oligoadenylate
XX PT synthetase, useful for treating a condition responsive to interferon-tau,
XX PT e.g. viral infection.
XX PS Claim 3; SEQ ID NO 2; 28pp; English.
XX CC The invention relates to a composition for use in treating a condition
XX CC responsive to interferon-tau, comprising an oral dosage form of interfeon
XX CC -tau. The composition is administered to a patient in a fasted state to
XX CC increase the level of 2',5'-oligoadenylate synthetase (OAS) in the blood
XX CC relative to that obtained after administration of interferon-tau to a fed
XX CC patient. The interferon-tau used in the composition is preferably ovine
XX CC or bovine. The composition is useful in the treatment of autoimmune
XX CC conditions (e.g., multiple sclerosis, diabetes mellitus, Hashimoto's
XX CC thyroiditis, rheumatoid arthritis, uveitis, psoriasis, systemic lupus
XX CC erythematosus, allergies, asthma, eczema, Crohn's disease or ulcerative
XX CC colitis), viral infections (e.g., HIV infection or hepatitis), disorders
XX CC associated with cellular proliferation (e.g., multiple myeloma, ovarian
XX CC cancer or hairy cell leukemia), or inflammatory diseases. The present
XX CC sequence represents mature ovine interferon-tau.
XX SQ
XX Sequence 172 AA;
XX Query Match 100.0%; Score 907; DB 7; Length 172;
XX Best Local Similarity 100.0%; Pred. No. 1e-92;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 KKYFGGIYDYLOEKYSDCAMEIVRVMRALTTVSTLLOKRLTMGGDLSNP 172
DB 121 KKYFGGIYDYLOEKYSDCAMEIVRVMRALTVSTLLOKRLTMGGDLSNP 172
XX
XX RESULT 7
XX ID ADM79177 standard; protein; 172 AA.
XX XX
XX ADM79177;
XX AC
XX 15-JUL-2004 (first entry)
XX DE Mature ovine interferon tau protein SEQ ID NO:1.
XX KM oral administration; interferon; IFN; ovine; mature interferon tau.
XX OS Ovis aries.
XX PN WO2004032863-A2.
XX PD 22-APR-2004.
XX PF 08-OCT-2003; 2003WO-US031999.
XX PR 09-OCT-2002; 2002US-0417292P.
XX PA (PEPG-) PEPGEN CORP.
XX PI Manning MC, Nayar R;
XX DR WPI; 2004-340799/31.
XX PT A composition for oral administration of an interferon (IFN) comprises an
XX PT IFN and a species that stabilizes the IFN in an active form by
XX PT interaction between the interferon and the species.
XX PS Example; SEQ ID NO 1; 52pp; English.
XX CC The present invention describes a composition for the oral administration
XX CC of an interferon (IFN) comprising an IFN and a species that stabilizes
XX CC the IFN in an active form by interaction between the IFN and the species.
XX CC Also described: (1) preparing a protein for oral administration,
XX CC comprising formulating the protein with a species that stabilizes the
XX CC protein in an active form by binding interaction between the protein and
XX CC the species, therefore the formulating results in a composition for oral
XX CC administration; and (2) selecting a dosage form composition for a protein
XX CC that achieves protein stabilization for biological activity upon in vivo
XX CC administration, comprising selecting a protein for formulation, preparing
XX CC solutions of the selected protein or polypeptide in different buffers at
XX CC different pH values, and measuring the effect of the buffer on the
XX CC protein's tertiary structure, where the measuring identifies buffers that
XX CC result retention of the protein's tertiary structure. The composition and
XX CC methods are useful for preparing oral dosage forms for administration of
XX CC proteins and polypeptides. The present sequence represents the mature
XX CC ovine interferon tau amino acid sequence, which is used in an example
XX CC from the present invention.
XX SQ
XX Sequence 172 AA;
XX Query Match 100.0%; Score 907; DB 8; Length 172;
XX Best Local Similarity 100.0%; Pred. No. 1e-92;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 KKYFGIYDYOEGKYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172
 DB 121 KKYFGIYDYOEGKYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172

RESULT 8
 ADS13613
 ID ADS13613 standard, protein, 172 AA.
 AC ADS13613;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Sheep interferon tau seqid 2.
 XX
 KW immunosuppressive; cytostatic; virucide; neuroprotective; antidiabetic;
 KW muscular; antiinflammatory; antirheumatic; antiarthritic; antiaesthetic;
 KW dermatological; vaccine; interferon tau; 2',5'-oligoadenylate synthetase;
 KW OAS; autoimmune condition; cancer; viral infection; multiple sclerosis;
 KW hepatitis C infection; diabetes mellitus; systemic lupus erythematosus;
 KW amyotrophic lateral sclerosis; Crohn's disease; rheumatoid arthritis;
 KW aethma; uveitis; psoriasis; hypersensitivity disorder; sheep.
 XX
 OS Ovis aries.
 OS
 PN US2004191217-A1.
 XX
 PD 30-SEP-2004.
 XX
 PE 21-NOV-2003; 2003US-00719472.
 XX
 PR 19-JUL-2000; 2000US-0219128P.
 PR 19-JUL-2001; 2001US-00910406.
 PR 16-JAN-2002; 2002US-0349658P.
 PR 16-JAN-2003; 2003US-00346269.
 PR 31-OCT-2003; 2003US-00698927.
 XX
 PA (SOKA/) SOKAMA Y.
 PA (LIUC/) LIU C.
 XX
 PI Sokawa Y, Liu C;
 XX
 DR WPI, 2004-698654/68.
 DR N-PSDB; ADS13612.
 XX
 PT Treating a condition in a subject, e.g. autoimmune condition, cancer or
 PT viral infection, comprises orally administering interferon-tau to the
 PT intestinal tract to increase the blood 2'5'-oligoadenylate synthetase
 PT level.
 XX
 PS Claim 2; SEQ ID NO 2; 38pp; English.
 XX
 CC The invention describes a method of creating a condition in a human
 CC subject responsive to interferon tau therapy comprises orally
 CC administering interferon-tau to the intestinal tract of the subject to
 CC produce an initial measurable increase in the subject's blood 2',5'-
 CC oligoadenylate synthetase (OAS) level, relative to the blood OAS level in
 CC the subject in the absence of interferon-tau administration. The method
 CC is useful for treating an autoimmune condition, cancer, or a viral
 CC infection. The method is particularly useful for treating multiple
 CC sclerosis or hepatitis C infection, diabetes mellitus, systemic lupus
 CC erythematosus, amyotrophic lateral sclerosis, Crohn's disease, rheumatoid
 CC arthritis, aethma, uveitis, psoriasis, and hypersensitivity disorders.
 CC This is the amino acid sequence of ovine interferon-tau.
 CC
 XX
 SQ Sequence 172 AA;
 QY Query Match 100.0%; Score 907; DB 8; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1e-92;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYLSRKLMLDARENKLLDRMNRSLPHSCLDRKDFGLPQEVNVEDQLOKQOAFVLYEM 60
 |||

DB 1 CYLSRKLMLDARENKLLDRMNRSLPHSCLDRKDFGLPQEVNVEDQLOKQOAFVLYEM 60
 QY 61 LQGSFNLFTYTHSSAAMDITLLLEQICTGLQQQLDHLDTCRGQVWGEEDSELGNMPIVTV 120
 DB 61 LQGSFNLFTYTHSSAAMDITLLLEQICTGLQQQLDHLDTCRGQVWGEEDSELGNMPIVTV 120

QY 121 KKYFGIYDYOEGKYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172
 DB 121 KKYFGIYDYOEGKYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172

RESULT 9
 AAR04540
 ID AAR04540 standard, protein, 195 AA.
 AC AAR04540;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-SEP-1990 (first entry)
 XX
 DE Ovine trophoblast protein-1 (bTP-1).
 KW Bovine trophoblast protein-1; bTP-1; fertility; ds.
 KW
 OS Sus scrofa.
 OS
 PN EP367063-A.
 XX
 PD 09-MAY-1990.
 XX
 PE 23-OCT-1989; 89EP-00119642.
 XX
 PR 26-OCT-1988; 88US-00262870.
 XX
 PA (UMOR) UNIV MISSOURI.
 PI Roberts MR, Imakawa K;
 XX
 DR WPI, 1990-141062/19.
 DR N-PSDB; AAO04289.
 XX
 PT Recombinant bovine trophoblast protein-1 - used for enhancing fertility
 PT or treating viral diseases in mammal, esp. cattle.
 XX
 PS Disclosure; Page ?; 27pp; English.
 XX
 CC The bTP-1 produced from the gene may be used to promote fertility or
 CC treat viral disease in cattle. The gene may also be used to provide
 CC transgenic animals with enhanced fertility, or in prophylactic and
 CC therapeutic treatment of other mammals. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 195 AA;
 QY Query Match 100.0%; Score 907; DB 2; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYLSRKLMLDARENKLLDRMNRSLPHSCLDRKDFGLPQEVNVEDQLOKQOAFVLYEM 60
 |||

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ID AAR09294 standard; protein; 172 AA.
XX
AC AAR09294;
XX
XX 25-MAR-2003 (revised)
DT 22-JAN-1991 (first entry)
XX
DE Ovine trophoblast protein-1.
XX
XX Interferon; tumour; virus; retrovirus; cancer; AIDS.
XX
OS Ovis aries.
XX
XX
FH Key Location/Qualifiers
FT Peptide 18..53
FT Peptide 68..76
FT Peptide 88..114
FT Peptide 130..138
FT Peptide 159..172
XX
XX WO9009806-A.
XX
XX 07-SEP-1990.
XX
XX 02-MAR-1989; 89US-00318050.
XX
XX 02-MAR-1989; 89US-00318050.
XX
XX (UYFL ) UNIV FLORIDA.
XX
XX Bazer FW, Johnson HM;
XX
XX WPI; 1990-290161/38.
XX
XX Non-cytotoxic inhibition of viruses and tumours - using conceptus-derived
PT ovine trophoblast protein-1.
XX
XX
XX Disclosure: Fig 1; 20pp; English.
XX
XX This conceptus-derived ovine trophoblast protein-1 (oTP-1) is used in a
CC compen. for inhibiting tumour growth or viral replic- action. It is an
CC interferon and exerts its inhibitory effect on viruses , retroviruses and
CC tumours without harming the cells of the host animal. Its fragments
CC (indicated in features) , or immunologically equivalent variants can also
CC be used. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX
XX Sequence 172 AA;
SQ
Query Match 99.8%; Score 905; DB 2; Length 172;
Best Local Similarity 99.4%; Pred. No. 1.7e-92;
Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYSRKMLDARENILKILDRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPPVLYEM 60
DB 1 CYSRKMLDARENILKILDRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPPVLYEM 60
QY 61 LQGSFNLPTTEHSSAAMDPTTLLLEQLCTGLQOQLDHLDTCRQVWGBEBSSELGNDPIYTV 120
DB 61 LQGSFNLPTTEHSSAAMDPTTLLLEQLCTGLQOQLDHLDTCRQVWGBEBSSELGNDPIYTV 120
QY 121 KKYFGIYDYLOEKGYSDCAMEIVVEMMRALTVSTTLQKRLTKMGDLSNP 172
DB 121 KKYFGIYDYLOEKGYSDCAMEIVVEMMRALTVSTTLQKRLTKMGDLSNP 172
RESULT 11
ID ADM79195 standard; protein; 172 AA.
XX
XX ADM79195;
XX
XX 15-JUL-2004 (first entry)
XX
```

```
DE Interferon tau protein.
XX
XX oral administration; interferon; IFN; mature interferon tau.
XX
XX Unidentified.
XX
XX WO2004032863-A2.
XX
XX 22-APR-2004.
XX
XX 08-OCT-2003; 2003WO-US031999.
XX
XX 09-OCT-2002; 2002US-0417292P.
XX
XX (PEPG-) PEPGEN CORP.
XX
XX Manning MC, Nayar R;
XX
XX WPI; 2004-340799/31.
XX
XX A composition for oral administration of an interferon (IFN) comprises an
PT IFN and a species that stabilizes the IFN in an active form by
PT interaction between the interferon and the species.
XX
XX Disclosure; Fig 1A; 52pp; English.
XX
XX The present invention describes a composition for the oral administration
CC of an interferon (IFN) comprising an IFN and a species that stabilizes
CC the IFN in an active form by interaction between the IFN and the species.
CC Also described: (1) preparing a protein for oral administration,
CC comprising formulating the protein with a species that stabilizes the
CC protein in an active form by binding interaction between the protein and
CC the species; therefore the formulating results in a composition for oral
CC administration; and (2) selecting a dosage form composition for a protein
CC that achieves protein stabilisation for biological activity upon in vivo
CC administration, comprising selecting a protein for formulation, preparing
CC solutions of the selected protein or polypeptide in different buffers at
CC different pH values, and measuring the effect of the buffer on the
CC protein's tertiary structure, where the measuring identifies buffers that
CC result retention of the protein's tertiary structure. The composition and
CC methods are useful for preparing oral dosage forms for administration of
CC proteins and polypeptides. The present sequence represents an interferon
CC tau amino acid sequence, which is used in the exemplification of the
CC present invention.
XX
XX
XX Sequence 172 AA;
SQ
Query Match 99.8%; Score 905; DB 8; Length 172;
Best Local Similarity 99.4%; Pred. No. 1.7e-92;
Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYSRKMLDARENILKILDRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPPVLYEM 60
DB 1 CYSRKMLDARENILKILDRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPPVLYEM 60
QY 61 LQGSFNLPTTEHSSAAMDPTTLLLEQLCTGLQOQLDHLDTCRQVWGBEBSSELGNDPIYTV 120
DB 61 LQGSFNLPTTEHSSAAMDPTTLLLEQLCTGLQOQLDHLDTCRQVWGBEBSSELGNDPIYTV 120
QY 121 KKYFGIYDYLOEKGYSDCAMEIVVEMMRALTVSTTLQKRLTKMGDLSNP 172
DB 121 KKYFGIYDYLOEKGYSDCAMEIVVEMMRALTVSTTLQKRLTKMGDLSNP 172
RESULT 12
ID AAR24942 standard; protein; 195 AA.
XX
XX AAR24942;
XX
XX 25-MAR-2003 (revised)
DT 03-JAN-1992 (first entry)
XX
```

```

DE Sequence of ovien trophoblastin variant Xa.
XX Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW trophoblastin; antitumolytic agent.
XX
XX Ammotragus lervia.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX FT /label= signal
XX
XX MO209691-A1.
XX
XX 11-JUN-1992.
XX
XX 29-NOV-1991; 91WO-FR000953.
XX
XX 29-NOV-1990; 90FR-00014945.
XX 29-NOV-1990; 90FR-00014946.
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
XX Martal J, Degryse E, Gaye P, Charlier M, Charpigny G, Reinaud P;
XX Chaouat G;
XX
XX WPI; 1992-217070/26.
XX
XX New type I interferon variants with added N-terminal dipeptide - include
XX expression cassettes providing high yield in yeast, esp. trophoblast
XX derivative, with e.g. anti-InteoLytic activity.
XX
XX Claim 7; Page 30; 53pp, French.
XX
XX The DNA sequence encoding the precursor of ovine trophoblastin was
XX disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
XX of trophoblastin. They have anti-InteoLytic activity and are used to
XX improve survival of transplanted embryos, as a reagent for detecting
XX viability of embryos at an early stage of its development; and to improve
XX the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 195 AA;
SQ
Query Match 99.7%; Score 904; DB 2; Length 195;
Best Local Similarity 99.4%; Fred. No. 2.7e-92;
Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CYLSRKMLDARENLKLDNRNRLSPHSCLODRKDFGLPOEMVEGDOLQXQAPFVLYEM 60
DB 24 CYLSRKMLDARENLKLDNRNRLSPHSCLODRKDFGLPOEMVEGDOLQXQAPFVLYEM 83
QY 61 LQGSFNLFTYHSSAAMDITLLLEOLCTGLQOQLDHLDTCRGOVMEEDSELGNDPIVTV 120
DB 84 LQGSFNLFTYHSSAAMDITLLDQLCTGLQOQLDHLDTCRGOVMEEDSELGNDPIVTV 143
QY 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
DB 144 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 195

```

```

KW ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KW colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KW monoclonal gammopathy; dysplasia; diabetes mellitus;
KW rheumatoid arthritis; lupus erythematosus.
XX
XX Ovis sp.
XX
XX MO200078266-A2.
XX
XX 28-DEC-2000.
XX
XX 22-JUN-2000; 2000MO-IB001080.
XX
XX 22-JUN-1999; 99US-0140411P.
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX
XX Pontzer CH, Shorts LH, Clark CD;
XX
XX WPI; 2001-071357/08.
XX N-PSDB; AAF24827.
XX
XX Producing recombinant interferon tau analog proteins with improved
XX properties, useful for treating cancers, autoimmune diseases and viral
XX infections.
XX
XX Claim 5; Page 59-60; 70pp; English.
XX
XX The present sequence represents an ovine interferon-tau 1mod polypeptide.
XX The specification describes a method of making recombinant interferon
XX (IFN)-tau proteins, which differ from wild-type IFN-tau by amino acid
XX substitutions near the amino terminus of the molecule. The mutated IFN-
XX tau proteins have improved biological activity, low toxicity, retain the
XX same or slightly reduced antiviral activity compared with interferon
XX alpha, and have enhanced antiproliferative activity compared to wild-type
XX IFN-tau. The method is used for producing IFN-tau proteins with improved
XX biological activities and properties. These IFN-tau may be administered
XX to treat cancers and decrease tumour growth, treat viral diseases, treat
XX autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
XX selected from the group comprising human adenocarcinoma, breast cancer,
XX prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
XX leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
XX cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
XX colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
XX gammopathies and cervical and oral dysplasia. The autoimmune disease is
XX selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
XX erythematosus and/or psoriasis. The viral infection is an RNA virus, a
XX human immuno deficiency virus (HIV) or hepatitis C virus
XX
XX Sequence 172 AA;
SQ
Query Match 99.2%; Score 900; DB 4; Length 172;
Best Local Similarity 99.4%; Fred. No. 6.3e-92;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CYLSRKMLDARENLKLDNRNRLSPHSCLODRKDFGLPOEMVEGDOLQXQAPFVLYEM 60
DB 1 CYLSRKMLDARENLKLDNRNRLSPHSCLODRKDFGLPOEMVEGDOLQXQAPFVLYEM 60
QY 61 LQGSFNLFTYHSSAAMDITLLLEOLCTGLQOQLDHLDTCRGOVMEEDSELGNDPIVTV 120
DB 61 LQGSFNLFTYHSSAAMDITLLLEOLCTGLQOQLDHLDTCRGOVMEEDSELGNDPIVTV 120
QY 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
DB 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172

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```

RESULT 14
AA021461
ID AA021461 standard; protein; 172 AA.
XX
XX AA021461;
AC

```

XX 15-AUG-2002 (first entry)
DT
XX
XX Ovine interferon-tau (OvIFN-tau) protein.
DE
XX Artificial ovine interferon-tau; OvIFN-tau; optimizing; biased codon;
KM high yield production.
XX
XX Ovis aries.
OS
XX Synthetic.
OS
XX MO200231178-A1.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001MO-US031862.
XX
XX 12-OCT-2000; 2000US-0239746P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Krishna R, Rodriguez E, Johnson H;
PI
XX WPI; 2002-426289/45.
DR
XX N-PSDB; AAL38060.
DR
XX
XX New artificial ovine interferon-tau gene, useful for high protein
PT production, constructed by reducing repetitive and palindromic sequences,
PT lowering overall guanine and cytosine content and optimizing gene
PT sequence.
XX
XX Disclosure; Fig 1A; 71pp; English.
PS
XX The invention relates to an artificial ovine interferon-tau (OvIFN-tau)
CC gene designed for high yield protein production in yeast, and constructed
CC by reducing repetitive sequences, lowering overall G+C content, reducing
CC or eliminating palindromic sequences, and optimizing the sequence of
CC OvIFN-tau, using the biased codon usage in the yeast. The expression
CC vector of the invention is useful for high yield production of OvIFN-tau
CC in the yeast of *Pichia*, preferably *P. pastoris* X33 or *P. pastoris* GS115,
CC by transforming the yeast with the expression vector, inducing protein
CC expression with methanol, culturing the yeast in defined culture
CC conditions such as shake flask or fermenter, and purifying the protein
CC from culture media. This sequence represents the ovine interferon-tau
CC (OvIFN-tau) protein of the invention
CC
XX
XX Sequence 172 AA;
SQ
Query Match 99.2%; Score 900; DB 5; Length 172;
Best Local Similarity 99.4%; Pred. No. 6.3e-92;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CYLSRKMLDARENKILDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPVLYEM 60
DB 1 CYLSRKMLDARENKILDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPVLYEM 60
OY 61 LOOSFNLFTYHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
DB 61 LOOSFNLFTYHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
OY 121 KKYFQGIYDYLOEKGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDLNSP 172
DB 121 KKYFQGIYDYLOEKGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDLNSP 172
RESULT 15
ABB07589
ID ABB07589 standard; protein; 172 AA.
XX
XX ABB07589;
AC
XX 08-MAY-2002 (first entry)
DT
XX

DE Recombinant ovine interferon-tau protein.
XX
XX Hepatitis C virus; HCV infection; ovine; interferon-tau; OvIFN-tau; OAS;
KM 2',5'-oligoadenylate synthetase; virucide; hepatotropic; IFN-tau.
XX
XX Ovis aries.
OS
XX MO200206343-A2.
XX
XX 24-JAN-2002.
XX
XX 19-JUL-2001; 2001MO-US022976.
XX
XX 19-JUL-2000; 2000US-0219128P.
PR 17-OCT-2000; 2000JP-00317160.
XX
XX (PEPG-) PEPGEN CORP.
XX
XX Sokawa Y, Liu C;
PI
XX WPI; 2002-179784/23.
DR
XX N-PSDB; ABA94937.
DR
XX
XX Oral-delivery composition for treating conditions relating to hepatitis
PT caused by hepatitis C virus, comprises ovine interferon-tau which
PT stimulates bloodstream levels of 2',5'-oligoadenylate synthetase.
XX
XX Example 1; Page 33; 33pp; English.
PS
XX
XX The invention provides an oral-delivery composition for use in treating
CC hepatitis C virus (HCV) in a HCV-infected patient. The composition
CC comprises ovine interferon-tau (OvIFN-tau), in a dosage effective to
CC stimulate bloodstream levels of 2',5'-oligoadenylate synthetase (OAS).
CC The OvIFN-tau synthesizes OAS which degrades viral mRNA. A method is also
CC provided for monitoring the treatment of HCV by oral administration of
CC OvIFN-tau, by measuring the blood levels of OAS prior to and after such
CC oral administration, and if necessary, adjusting the dose of IFN-tau
CC until a measurable increase in blood OAS level, relative to the level
CC observed prior to administration. The composition is useful for treating
CC hepatitis caused by HCV and the method is useful for monitoring treatment
CC of HCV by oral administration of OvIFN-tau. The present sequence
CC represents a recombinant ovine interferon-tau protein
CC
XX
XX Sequence 172 AA;
SQ
Query Match 99.1%; Score 899; DB 5; Length 172;
Best Local Similarity 98.8%; Pred. No. 8.1e-92;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 CYLSRKMLDARENKILDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPVLYEM 60
DB 1 CYLSERKMLDARENKILDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPVLYEM 60
OY 61 LOOSFNLFTYHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
DB 61 LOOSFNLFTYHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
OY 121 KKYFQGIYDYLOEKGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDLNSP 172
DB 121 KKYFQGIYDYLOEKGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDLNSP 172
RESULT 16
ADM79178
ID ADM79178 standard; protein; 172 AA.
XX
XX ADM79178;
AC
XX 15-JUL-2004 (first entry)
DT
XX Mature ovine interferon tau variant protein SEQ ID NO:2.
DE
XX oral administration; interferon; IFN; ovine; mature interferon tau;
KM

QY 121 KKYFGIYDYLOEKGYSDCAMEIVRVMRALTVSTTLQKRLTKMGDLNSP 172
 DB 121 KKYFGIYDYLOEKGYSDCAMEIVRVMRALTVSTTLQKRLTKMGDLNSP 172

RESULT 18 AAB31462

ID AAB31462 standard; protein; 172 AA.

AC AAB31462;

DT 20-APR-2001 (first entry)

DE An ovine interferon-tau lmod polypeptide with mutation L241.

Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
 lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
 colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
 monoclonal gammopathy; dysplasia; diabetes mellitus;
 rheumatoid arthritis; lupus erythematosus.

Synthetic.

OS Ovis sp.

PN WO200078266-A2.

PD 28-DEC-2000.

PF 22-JUN-2000; 2000WO-IB001080.

PR 22-JUN-1999; 99US-0140411P.

PA (UYMA-) UNIV MARYLAND BALTIMORE.

PI Pontzer CH, Shortes LH, Clark CD;

DR WPI; 2001-071357/08.

DR N-PSDB; AAF24831.

PT Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.

PS Claim 15; Page 64; 70pp; English.

The present sequence represents a mutated ovine interferon-tau lmod
 polypeptide, which was made using the method of the invention. The
 specification describes a method of making recombinant interferon (IFN)-
 tau proteins, which differ from wild-type IFN-tau by amino acid
 substitutions near the amino terminus of the molecule. The mutated IFN-
 tau proteins have improved biological activity, low toxicity, retain the
 same or slightly enhanced antiviral activity compared with interferon
 alpha, and have enhanced antiproliferative activity compared to wild-type
 IFN-tau. The method is used for producing IFN-tau proteins with improved
 biological activities and properties. These IFN-tau may be administered
 to treat cancers and decrease tumour growth, treat viral diseases, treat
 autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 selected from the group comprising human adenocarcinoma, breast cancer,
 prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
 gammopathies and cervical and oral dysplasia. The autoimmune disease is
 selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 human immuno deficiency virus (HIV) or hepatitis C virus

Sequence 172 AA;

Query Match 99.0%; Score 898; DB 4; Length 172;

Best Local Similarity 98.8%; Pred. No. 1e-91;
 Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYLSRKILMDARENLKILDMNRISPHSCIQDRKDFGLPOBMEVGDQLQDAFPVLYEM 60

DB 1 CYLSRKILMDARENLKILDMNRISPHSCIQDRKDFGLPOBMEVGDQLQDAFPVLYEM 60

QY 61 LQOSFNLPTHESSAANDTTLLEQLCTGLQOQDLHDTCTCGQVNGEEDSELGNNDPIVTV 120

DB 61 LQOSFNLPTHESSAANDTTLLEQLCTGLQOQDLHDTCTCGQVNGEEDSELGNNDPIVTV 120

QY 121 KKYFGIYDYLOEKGYSDCAMEIVRVMRALTVSTTLQKRLTKMGDLNSP 172

DB 121 KKYFGIYDYLOEKGYSDCAMEIVRVMRALTVSTTLQKRLTKMGDLNSP 172

RESULT 19 AAR24941

ID AAR24941 standard; protein; 195 AA.

AC AAR24941;

DT 25-MAR-2003 (revised)

DT 03-JAN-1992 (first entry)

DE Sequence of ovine trophoblastin.

Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;

trophoblastin; antileukolytic agent.

OS Ammotragus lervia.

EH Key Location/Qualifiers

FT Peptide 1..23

FT /label= signal

PN WO9209691-A1.

PD 11-JUN-1992.

PF 29-NOV-1991; 91WO-FR000953.

PR 29-NOV-1990; 90FR-00014945.

PR 29-NOV-1990; 90FR-00014946.

PA (INRG) INRA INST NAT RECH AGRONOMICUE.

PI Martal J, Degryse E, Gaye P, Charlier M, Charpigny G, Renaud P;

PI Chaouat G;

DR WPI; 1992-217070/26.

New type I interferon variants with added N-terminal dipeptide - include
 PT expression cassettes providing high yield in yeast, esp. trophoblast
 PT derive. with e.g. anti-leukolytic activity.

PS Disclosure; Fig 1; 53pp; French.

The DNA sequence encoding the precursor of ovine trophoblastin was
 CC disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
 CC of trophoblastin. They have anti-leukolytic activity and are used to
 CC improve survival of transplanted embryos; as a reagent for detecting
 CC viability of embryos at an early stage of its development; and to improve
 CC the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 195 AA;

Query Match 98.9%; Score 897; DB 2; Length 195;
 Best Local Similarity 98.3%; Pred. No. 1.6e-91;
 Matches 169; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYLSRKILMDARENLKILDMNRISPHSCIQDRKDFGLPOBMEVGDQLQDAFPVLYEM 60
 |||||:|||||

```

Db      24  CYLSORLMLDARENKLLDRMNRSLSPHSCLODRKDFGLPEQWVEGDQLQKQAFVLYEM 83
Oy      61  LQGSFNLFTYTHSSAAMDITLLLEQLCTGILQOQLDHLDTCRGQVWGEEDSELGNDPIVTV 120
Db      84  LQGSFNLFTYTHSSAAMDITLLDQLCTGILQOQLDHLDTCRGQVWGEEDSELGNDPIVTV 143
Oy      121 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
Db      144 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 195

RESULT 20
AAR24945
ID      AAR24945 standard; protein; 195 AA.
XX
XX      AAR24945;
AC
XX      25-MAR-2003 (revised)
DT      03-JAN-1992 (first entry)
XX
XX      Sequence of ovine trophoblastin variant Xd.
DE
XX      Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW      trophoblastin; antileukolytic agent.
XX
XX      Ammocreagus lervia.
OS
XX
XX      Key      Location/Qualifiers
FH      Peptide 1..23
FT      /label= signal
XX
XX      WO9209691-A1.
XX
XX      11-JUN-1992.
PD
XX      29-NOV-1991; 91WO-FR000953.
PF
XX      29-NOV-1990; 90FR-00014945.
PR      29-NOV-1990; 90FR-00014946.
XX
XX      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA
XX      Martal J, Degryse E, Gage P, Charlier M, Charpigny G, Reinaud P;
PI      Chaouat G;
XX
XX      WPI; 1992-217070/26.
DR
XX
XX      New type I interferon variants with added N-terminal dipeptide - include
PT      expression cassettes providing high yield in yeast, esp. trophoblast
PT      derivative, with e.g. anti-leukolytic activity.
XX
XX      Claim 7; Page 30; 53pp; French.
XX
XX      The DNA sequence encoding the precursor of ovine trophoblastin was
CC      disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
CC      of trophoblastin. They have anti-leukolytic activity and are used to
CC      improve survival of transplanted embryos; as a reagent for detecting
CC      viability of embryos at an early stage of its development; and to improve
CC      the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX      Sequence 195 AA:
SQ
Query Match 98.9%; Score 897; DB 2; Length 195;
Best Local Similarity 98.3%; Pred. No. 1,6e-91;
Matches 169; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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```

Oy      121 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
Db      144 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 195

RESULT 21
AAB31468
ID      AAB31468 standard; protein; 172 AA.
XX
XX      AAB31468;
AC
XX      20-APR-2001 (first entry)
DT
XX
XX      An ovine interferon-tau Imod polypeptide with mutation R20Q.
DE
XX
XX      Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
KW      autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
KW      prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
KW      lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
KW      ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KW      colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KW      monoclonal gammopathy; dysplasia; diabetes mellitus;
KW      rheumatoid arthritis; lupus erythematosus.
XX
XX      Synthetic.
OS
XX      Ovis sp.
XX
XX      WO200078266-A2.
XX
XX      28-DEC-2000.
PD
XX      22-JUN-2000; 2000WO-IB001080.
PF
XX      22-JUN-1999; 99US-0140411P.
PR
XX
XX      (UTMA-) UNIV MARYLAND BALTIMORE.
PA
XX      Pontzer CH, Shorts LH, Clark CD;
PI
XX
XX      WPI; 2001-071357/08.
DR
XX
XX      Producing recombinant interferon tau analog proteins with improved
PT      properties, useful for treating cancers, autoimmune diseases and viral
PT      infections.
XX
XX      Claim 15; Page 69-70; 70pp; English.
XX
XX      The present sequence represents a mutated ovine interferon-tau Imod
CC      polypeptide, which was made using the method of the invention. The
CC      specification describes a method of making recombinant interferon (IFN)-
CC      tau proteins, which differ from wild-type IFN-tau by amino acid
CC      substitutions near the amino terminus of the molecule. The mutated IFN-
CC      tau proteins have improved biological activity, low toxicity, retain the
CC      same or slightly reduced antiviral activity compared with interferon
CC      alpha, and have enhanced antiproliferative activity compared to wild-type
CC      IFN-tau. The method is used for producing IFN-tau proteins with improved
CC      biological activities and properties. These IFN-tau may be administered
CC      to treat cancers and decrease tumour growth, treat viral diseases, treat
CC      autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
CC      selected from the group comprising human adenocarcinoma, breast cancer,
CC      prostate cancer, glioblastoma, melanoma, myeloma, lymphoma,
CC      leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
CC      cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
CC      colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
CC      gammopathies and cervical and oral dysplasia. The autoimmune disease is
CC      selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
CC      erythematosus and/or psoriasis. The viral infection is an RNA virus, a
CC      human immunodeficiency virus (HIV) or hepatitis C virus
XX
XX      Sequence 172 AA:
SQ
Query Match 98.8%; Score 896; DB 4; Length 172;

```

Best Local Similarity 98.8%; Pred. No. 1.8e-91;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVEGDQLOKQAFPVLYEM 60
DB 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVEGDQLOKQAFPVLYEM 60
QY 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRGQGGEEDSELGNMDPIVTV 120
DB 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRGQGGEEDSELGNMDPIVTV 120
QY 121 KKYFGIYDYLQEKGYSDCAMEIVRVEMRALTVSTTLQKRLTVMGDLNSP 172
DB 121 KKYFGIYDYLQEKGYSDCAMEIVRVEMRALTVSTTLQKRLTVMGDLNSP 172

RESULT 22
AAB31466 standard; protein; 172 AA.

AC AAB31466;
XX
DT 20-APR-2001 (first entry)
XX
DE An ovine interferon-tau 1mod polypeptide with mutation R5Q.
XX
KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KM monoclonal gammopathy; dysplasia; diabetes mellitus;
KM rheumatoid arthritis; lupus erythematosus.
KM
XX
OS Synthetic.
OS Ovis sp.
XX
PN WO200078266-A2.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-2000; 2000WO-IB001080.
XX
PR 22-JUN-1999; 99US-0140411P.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Pontzer CH, Shorts LH, Clark CD;
XX
DR WPI; 2001-071357/08.
XX
PT producing recombinant interferon tau analog proteins with improved
PT properties, useful for treating cancers, autoimmune diseases and viral
PT infections.
XX
PS Claim 15; Page 67-68; 70pp; English.

CC The present sequence represents a mutated ovine interferon-tau 1mod
CC polypeptide, which was made using the method of the invention. The
CC specification describes a method of making recombinant interferon (IFN)-
CC tau proteins, which differ from wild-type IFN-tau by amino acid
CC substitutions near the amino terminus of the molecule. The mutated IFN-
CC tau proteins have improved biological activity, low toxicity, retain the
CC same or slightly reduced antiviral activity compared with interferon
CC alpha, and have enhanced antiproliferative activity compared to wild-type
CC IFN-tau. The method is used for producing IFN-tau proteins with improved
CC biological activities and properties. These IFN-tau may be administered
CC to treat cancers and decrease tumour growth, treat viral diseases, treat
CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
CC selected from the group comprising human adenocarcinoma, breast cancer,
CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain

CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
CC colorectal cancer, cervical cancer and neuroectodermal cancer; monoclonal
CC gammopathies and cervical and oral dysplasia. The autoimmune disease is
CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
CC human immuno deficiency virus (HIV) or hepatitis C virus
XX

SQ Sequence 172 AA;
Query Match 98.8%; Score 896; DB 4; Length 172;
Best Local Similarity 98.8%; Pred. No. 1.8e-91;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVEGDQLOKQAFPVLYEM 60
DB 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVEGDQLOKQAFPVLYEM 60
QY 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRGQGGEEDSELGNMDPIVTV 120
DB 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRGQGGEEDSELGNMDPIVTV 120
QY 121 KKYFGIYDYLQEKGYSDCAMEIVRVEMRALTVSTTLQKRLTVMGDLNSP 172
DB 121 KKYFGIYDYLQEKGYSDCAMEIVRVEMRALTVSTTLQKRLTVMGDLNSP 172

RESULT 23
AAB31464 standard; protein; 172 AA.

ID AAB31464;
XX
AC AAB31464;
XX
DT 20-APR-2001 (first entry)
XX
DE An ovine interferon-tau 1mod polypeptide with mutation Q31K.
XX
KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KM monoclonal gammopathy; dysplasia; diabetes mellitus;
KM rheumatoid arthritis; lupus erythematosus.
KM
XX
OS Synthetic.
OS Ovis sp.
XX
PN WO200078266-A2.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-2000; 2000WO-IB001080.
XX
PR 22-JUN-1999; 99US-0140411P.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Pontzer CH, Shorts LH, Clark CD;
XX
DR WPI; 2001-071357/08.
XX
PF N-PSDB; AAF24833.
XX
PT producing recombinant interferon tau analog proteins with improved
PT properties, useful for treating cancers, autoimmune diseases and viral
PT infections.
XX
PS Claim 15; Page 65-66; 70pp; English.

CC The present sequence represents a mutated ovine interferon-tau 1mod
CC polypeptide, which was made using the method of the invention. The
CC specification describes a method of making recombinant interferon (IFN)-
CC tau proteins, which differ from wild-type IFN-tau by amino acid

XX 22-JUN-2000; 2000MO-IB001080.
 XX 22-JUN-1999; 99US-0140411P.
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 XX Pontzer CH, Shorte LH, Clark CD;
 XX WPI; 2001-071357/08.
 XX Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.
 XX Claim 15; Page 68-69; 70pp; English.
 XX The present sequence represents a mutated ovine interferon-tau lmod
 CC polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
 CC gammaglobulins and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 CC human immuno deficiency virus (HIV) or hepatitis C virus
 XX
 SQ Sequence 172 AA;
 Query Match 98.6%; Score 894; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 2.9e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVBDQLQKQAPFVLYEM 60
 DB 1 CYLSRTMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVBDQLQKQAPFVLYEM 60
 QY 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHDLTCRQGVNGEBSDELGNNDPIVTV 120
 DB 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHDLTCRQGVNGEBSDELGNNDPIVTV 120
 QY 121 KKYFGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLLTXMGDLSNP 172
 DB 121 KKYFGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLLTXMGDLSNP 172
 RESULT 26
 AAB31465 ID AAB31465 standard; protein; 172 AA.
 XX AAB31465;
 XX 20-APR-2001 (first entry)
 XX An ovine interferon-tau lmod polypeptide with mutation K34H.
 XX Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 KW autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 KW prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
 KW lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 KW ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;

KW colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
 KW monoclonal gammopathy; dysplasia; diabetes mellitus;
 KW rheumatoid arthritis; lupus erythematosus.
 OS Synthetic.
 OS Ovis sp.
 XX WO200078266-A2.
 XX 28-DEC-2000.
 XX 22-JUN-2000; 2000MO-IB001080.
 XX 22-JUN-1999; 99US-0140411P.
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 XX Pontzer CH, Shorte LH, Clark CD;
 XX WPI; 2001-071357/08.
 XX N-PSDB; AAF24834.
 XX Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.
 XX Claim 15; Page 66-67; 70pp; English.
 XX The present sequence represents a mutated ovine interferon-tau lmod
 CC polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
 CC gammaglobulins and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 CC human immuno deficiency virus (HIV) or hepatitis C virus
 XX
 SQ Sequence 172 AA;
 Query Match 98.6%; Score 894; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 2.9e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVBDQLQKQAPFVLYEM 60
 DB 1 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVBDQLQKQAPFVLYEM 60
 QY 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHDLTCRQGVNGEBSDELGNNDPIVTV 120
 DB 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHDLTCRQGVNGEBSDELGNNDPIVTV 120
 QY 121 KKYFGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLLTXMGDLSNP 172
 DB 121 KKYFGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLLTXMGDLSNP 172
 RESULT 27
 AAB31460 ID AAB31460 standard; protein; 172 AA.
 XX

AC AAB31460;
 XX
 XX 20-APR-2001 (first entry)
 DT
 DE An ovine interferon-tau 1mod polypeptide with mutation K16M.
 XX
 KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 KM prostate cancer; glioblastoma; melanoma; lymphoma; leukaemia;
 KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
 KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
 KM monoclonal gammopathy; dysplasia; diabetes mellitus;
 KM rheumatoid arthritis; lupus erythematosus.
 KM
 XX Synthetic.
 OS
 OS Ovis sp.
 XX
 XX WO200078266-A2.
 XX
 XX 28-DEC-2000.
 PD
 XX 22-JUN-2000; 2000WO-IB001080.
 PF
 XX 22-JUN-1999; 99US-014041P.
 PR
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 PA
 PI Pontzer CH, Shorts LH, Clark CD;
 DR WPI: 2001-071357/08.
 DR N-PSDB; AAF24829.
 XX
 PT Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.
 PT
 XX
 XX Claim 15; Page 62-63; 70pp; English.
 PS
 XX The present sequence represents a mutated ovine interferon-tau 1mod
 CC polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastoma, melanomas, myelomas, lymphomas,
 CC leukemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
 CC gammopathies and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 CC human immuno deficiency virus (HIV) or hepatitis C virus
 CC
 XX
 SQ Sequence 172 AA;
 Query Match 98.6%; Score 894; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 2.9e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 61 LQSFNLFYTHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRGQVGEEDSEIGNMDPIYTV 120
 QY 121 KKYFGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
 DB 121 KKYFGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
 DB
 RESULT 28
 AAR24944
 ID AAR24944 standard; protein; 195 AA.
 XX
 AC AAR24944;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-JAN-1992 (first entry)
 XX
 DE Sequence of ovine trophoblastin variant Xc.
 KM Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
 KM trophoblastin; antileukolytic agent.
 XX
 OS Ammotragus lervia.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..23
 FT /label= signal
 XX
 PN WO9209691-A1.
 XX
 PD 11-JUN-1992.
 XX
 XX 29-NOV-1991; 91WO-FR000953.
 PF
 XX 29-NOV-1990; 90FR-00014945.
 PR 29-NOV-1990; 90FR-00014946.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX
 PI Martal J, Degryse E, Gaye P, Charlier M, Charpigny G, Reinaud P;
 PI Chaouat G;
 DR WPI: 1992-217070/26.
 XX
 XX New type I interferon variants with added N-terminal dipeptide - include
 PT expression cassettes providing high yield in yeast, esp. trophoblast
 PT derive, with e.g. anti-leukolytic activity.
 PT
 XX
 PS Claim 7; Page 30; 53pp; French.
 XX
 CC The DNA sequence encoding the precursor of ovine trophoblastin was
 CC disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
 CC of trophoblastin. They have anti-leukolytic activity and are used to
 CC improve survival of transplanted embryos; as a reagent for detecting
 CC viability of embryos at an early stage of its development; and to improve
 CC the fertility of livestock. (updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 195 AA;
 Query Match 98.6%; Score 894; DB 2; Length 195;
 Best Local Similarity 97.7%; Pred. No. 3.5e-91;
 Matches 168; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 29
 AAB31461
 ID AAB31461 standard; protein, 172 AA.
 AC AAB31461;
 XX
 DT 20-APR-2001 (first entry)
 DE An ovine interferon-tau lmod polypeptide with mutation D19A.
 XX
 KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
 KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
 KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
 KM monoclonal gammopathy; dysplasia; diabetes mellitus;
 KM rheumatoid arthritis; lupus erythematosus.
 KM
 OS Synthetic.
 OS Ovis sp.
 PN MO200078266-A2.
 PD 28-DEC-2000.
 XX
 PF 22-JUN-2000; 2000WO-IB001080.
 XX
 PR 22-JUN-1999; 99US-0140411P.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 P1 Pontzer CH, Shorte LH, Clark CD;
 XX
 DR WPI; 2001-071357/08.
 DR N-PSDB; AAF24830.
 PT Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.
 PS Claim 15; Page 63; 70pp; English.
 XX
 CC The present sequence represents a mutated ovine interferon-tau lmod
 CC polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
 CC gammopathies and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 CC human immunodeficiency virus (HIV) or hepatitis C virus
 CC
 SO Sequence 172 AA;
 Query Match 98.3%; Score 892; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 4.9e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYLSRKIMLDARENLKLLDBMNRSLPHSCLODRKDFGLPOEMVEGDLOKQDAFPVLYEM 60
 DB 1 CYLSRKIMLDARENLKLLARNRSLPHSCLODRKDFGLPOEMVEGDLOKQDAFPVLYEM 60
 QY 61 LOOSFNLFTYHSSAAMDITLLBQLCTGLOOQDLHDLDTCRGQVGEBSDELGNMDFIVTV 120
 DB 61 LOOSFNLFTYHSSAAMDITLLBQLCTGLOOQDLHDLDTCRGQVGEBSDELGNMDFIVTV 120
 QY 121 KRYFGIYDYLOEKGYSDCAMEIYRVEMRALTSTTLQRLTGMGDLNSP 172
 DB 121 KRYFGIYDYLOEKGYSDCAMEIYRVEMRALTSTTLQRLTGMGDLNSP 172
 RESULT 30
 AAB31463
 ID AAB31463 standard; protein, 172 AA.
 AC AAB31463;
 XX
 DT 20-APR-2001 (first entry)
 DE An ovine interferon-tau lmod polypeptide with mutation P26L.
 XX
 KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
 KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
 KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
 KM monoclonal gammopathy; dysplasia; diabetes mellitus;
 KM rheumatoid arthritis; lupus erythematosus.
 KM
 OS Synthetic.
 OS Ovis sp.
 PN MO200078266-A2.
 PD 28-DEC-2000.
 XX
 PF 22-JUN-2000; 2000WO-IB001080.
 XX
 PR 22-JUN-1999; 99US-0140411P.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 P1 Pontzer CH, Shorte LH, Clark CD;
 XX
 DR WPI; 2001-071357/08.
 DR N-PSDB; AAF24832.
 PT Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.
 PS Claim 15; Page 64-65; 70pp; English.
 XX
 CC The present sequence represents a mutated ovine interferon-tau lmod
 CC polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal

CC gammaglobulins and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematous and/or psoriasis. The viral infection is an RNA virus, a
 CC human immunodeficiency virus (HIV) or hepatitis C virus
 XX
 SO Sequence 172 AA:

Query Match 98.1%; Score 890; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 8.2e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CYLSRKMLDARENKILDRNRLSPHSCLDRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
 DB 1 CYLSRKMLDARENKILDRNRLSPHSCLDRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
 OY 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHLDTCRGQVGEEDSELGNMDPIVTV 120
 DB 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHLDTCRGQVGEEDSELGNMDPIVTV 120
 OY 121 KKYFGIYDYLQEKGYSDCAWEIVREVMRALTVSTTLQKRLTKKGDLNSP 172
 DB 121 KKYFGIYDYLQEKGYSDCAWEIVREVMRALTVSTTLQKRLTKKGDLNSP 172

RESULT 31

AAP91396
 ID AAP91396 standard; protein; 195 AA.

XX AAP91396;

XX 25-MAR-2003 (revised)
 DT 15-FEB-1990 (first entry)

XX Isoform of Class II alpha-interferon trophoblastine precursor.

XX Antiviral; antitumour.

XX Unidentified.

XX WO8908706-A.

XX 21-SEP-1989.

XX 17-MAR-1989; 89WO-FR000116.

XX 31-JAN-1989; 89US-00304209.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PI Martal J, Charpigny G, Gaye P, Pernollet J, Charlier M;
 PI Guillomot M, Huet JC, Reinaud P;

DR WPI; 1989-292521/40.

PT New isoform(s) of the class II alpha interferon trophoblastine - with
 PT e.g. antiviral, antitumour and immuno-modulating activities, and new DNA
 PT encoding sequences.

PS Claim 11; Page 11; 47pp; French.

XX The isoform (23 kD) can be used for immunological, rejection-inhibiting,
 CC and cell differentiation activities. It can inhibit interleukins at the
 CC start of pregnancy, monitor embryo viability, and protect embryos during
 CC transfer to the womb of a recipient. (Updated on 25-MAR-2003 to correct
 CC PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)

XX Sequence 195 AA:

Query Match 97.4%; Score 883; DB 1; Length 195;
 Best Local Similarity 97.1%; Pred. No. 5.9e-90;
 Matches 167; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYLSRKMLDARENKILDRNRLSPHSCLDRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
 DB 24 CYLSRKMLDARENKILDRNRLSPHSCLDRKDFGLPQEMVSGDQLQKQAPFVLYEM 83
 OY 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHLDTCRGQVGEEDSELGNMDPIVTV 120
 DB 84 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHLDTCRGQVGEEDSELGNMDPIVTV 143
 OY 121 KKYFGIYDYLQEKGYSDCAWEIVREVMRALTVSTTLQKRLTKKGDLNSP 172
 DB 144 KKYFGIYDYLQEKGYSDCAWEIVREVMRALTVSTTLQKRLTKKGDLNSP 195

RESULT 32

AAR24943
 ID AAR24943 standard; protein; 195 AA.

XX AAR24943;

XX 25-MAR-2003 (revised)
 DT 03-JAN-1992 (first entry)

XX Sequence of ovine trophoblastin variant Xb.

XX Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
 KM trophoblastin; antileukolytic agent.

XX Ammotragus lervia.

XX Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal

XX WO9209691-A1.

XX 11-JUN-1992.

XX 29-NOV-1991; 91WO-FR000953.

XX 29-NOV-1990; 90FR-00014945.

XX 29-NOV-1990; 90FR-00014946.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PI Martal J, Degryse B, Gaye P, Charlier M, Charpigny G, Reinaud P;
 PI Chaouat G;

DR WPI; 1992-217070/26.

PT New type I interferon variants with added N-terminal dipeptide - include
 PT expression cassettes providing high yield in yeast, esp. trophoblast
 PT derivative, with e.g. anti-leukolytic activity.

PS Claim 7; Page 30; 53pp; French.

XX The DNA sequence encoding the precursor of ovine trophoblastin was
 CC disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
 CC of trophoblastin. They have anti-leukolytic activity and are used to
 CC improve survival of transplanted embryos; as a reagent for detecting
 CC viability of embryos at an early stage of its development; and to improve
 CC the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 195 AA:

Query Match 96.4%; Score 874; DB 2; Length 195;
 Best Local Similarity 96.5%; Pred. No. 6e-89;
 Matches 166; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 CYLSRKMLDARENKILDRNRLSPHSCLDRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
 DB 24 CYLSRKMLDARENKILDRNRLSPHSCLDRKDFGLPQEMVSGDQLQKQAPFVLYEM 83
 OY 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHLDTCRGQVGEEDSELGNMDPIVTV 120

```

Db      84 LQGSFNLFTYEHSSAAMDITLLDQCTGLQQQLDHLDTCCRGQVMGEEDSELGNDPIYTV 143
Oy      121 KKXFGIYDYLOEKGYSDCAMEIVRVEMRALTVSTTLQKRLTKMGDLNSP 172
Db      144 KKXFGIYDYLOEKGYSDCAMEIVRVEMRALTVSTTLQKRLTKMGDLNSP 195

RESULT 33
AAB49784
ID AAB49784 standard; protein; 196 AA.
XX
AC AAB49784;
XX
DT 23-APR-2001 (first entry)
XX
DE Ovi TP-1 amino acid sequence.
XX
KW Human; keratinocyte derived interferon; KDI; viral infection; lymphoma;
KW immune system related disorder; cancer; multiple sclerosis; AIDS;
KW hepatitis; Cryptosporidium parvum infection; leukaemia; arthritis;
KW diabetes; allergy; chronic myelogenous leukaemia.
XX
OS Synthetic.
XX
PN WO200107608-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JAN-2000; 2000WO-US001239.
XX
PR 21-JUL-1999; 99US-00358587.
PR 21-JUL-1999; 99WO-US016424.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Moore PA, Lafleur DW;
XX
DR WPI; 2001-138557/14.
XX
PT Isolated keratinocyte derived interferon protein and polynucleotide used
PT to prevent, treat or ameliorate an immune system-related disorder, viral
PT infection, viral exposure and cancer.
XX
PS Disclosure; Fig 4; 303pp; English.
XX
XX
CC This invention relates to human polynucleotide sequence AAF72333 which
CC encodes keratinocyte derived interferon (KDI) protein AAB49774, which is
CC a member of the interferon family. AAF72338 represents the codon
CC optimised sequence of KDI. The human KDI gene is located on chromosome 9.
CC The specification includes KDI related protein sequences AAB49775 -
CC AAB49789. Also given in the specification are primer, probe and
CC polynucleotide sequences represented by AAF72334-AAF72370 (excluding
CC AAF72338) which are used in the isolation and characterisation of the KDI
CC sequence of the invention. The KDI polypeptide is used to treat viral
CC infections and the protein and polynucleotide may be used to prevent,
CC treat or ameliorate a medical condition such as immune system-related
CC disorder, viral infection, viral exposure and cancer in a mammal.
CC Specific disorders which can be treated by KDI include multiple
CC sclerosis, lymphoma, acquired immune deficiency syndrome, viral
CC hepatitis, Cryptosporidium parvum infection, chronic myelogenous
CC leukaemia, arthritis, diabetes and allergies
XX
SQ Sequence 196 AA:

Query Match      94.5%; Score 857.5; DB 4; Length 196;
Best Local Similarity 94.8%; Pred. No. 4.2e-87;
Matches 164; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

```

```

Oy      61 LQGSFNLFTYEHSSAAMDITLLDQCTGLQQQLDHLDTCCRGQVMGEEDSELGNDPIYTV 119
Db      84 LQGSFNLFTYEHSSAAMDITLLDQCTGLQQQLDHLDTCCRGQVMGEEDSELGNDPIYTV 143
Oy      120 VKKXFGIYDYLOEKGYSDCAMEIVRVEMRALTVSTTLQKRLTKMGDLNSP 172
Db      144 VKKXFGIYDYLOEKGYSDCAMEIVRVEMRALTVSTTLQKRLTKMGDLNSP 196

RESULT 34
ADF94976
ID ADF94976 standard; protein; 196 AA.
XX
AC ADF94976;
XX
DT 26-FEB-2004 (first entry)
XX
DE Sheep IFN homologue, TP-1, SEQ ID:12.
XX
KW Human keratinocyte derived interferon; human KDI; agonist; antagonist;
KW binding partner identification; immune-related disorder; cancer;
KW viral infection; viral exposure; immunomodulator; virucide; cytostatic;
KW gene therapy; TP-1; ovine; sheep.
XX
OS Ovis aries.
XX
PN WO2003031566-A2.
XX
PD 17-APR-2003.
XX
PF 19-JUL-2002; 2002WO-US023214.
XX
PR 20-JUL-2001; 2001US-00908594.
PR 06-DEC-2001; 2001US-0336165P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Lafleur DW, Moore PA, Ruben SM;
XX
DR WPI; 2003-381702/36.
XX
PT New isolated keratinocyte derived interferon (KDI) polypeptide, useful
PT for preventing, treating or ameliorating a medical condition, such as an
PT immune-related disorder, a viral infection, a viral exposure or cancer.
XX
PS Disclosure; SEQ ID NO 12; 398pp; English.
XX
XX
CC The invention relates to human keratinocyte derived interferon (KDI;
CC ADF94966) and nucleic acids encoding it (ADF94965). The KDI gene is
CC located on chromosome 9q22. The invention also relates to sequences at
CC least 70% identical to the KDI nucleic acid and protein sequences; a
CC polypeptide comprising an epitope-bearing portion of KDI; recombinant
CC vectors and host cells comprising a KDI nucleic acid sequence; a method
CC for the recombinant expression of KDI proteins; a KDI-specific antibody;
CC KDI agonists and antagonists; use of KDI nucleic acids or proteins for
CC treating medical conditions; a method for the diagnosis of a pathological
CC condition or susceptibility to a pathological condition; and methods of
CC screening for KDI binding partners. The KDI polypeptides and
CC polynucleotides, and methods of the invention are useful for preventing,
CC treating or ameliorating a medical condition, such as an immune-related
CC disorder, cancer, or a viral infection or viral exposure. The present
CC sequence is related to the invention.
XX
SQ Sequence 196 AA:

Query Match      94.5%; Score 857.5; DB 7; Length 196;
Best Local Similarity 94.8%; Pred. No. 4.2e-87;
Matches 164; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

```

```

QY 61 LOOSFNLFTYTHSSAAMDPTTLEQLCTGLQOQDLHLDTCRGVWGEEDSELGNMDEPIVTV 119
DB 84 LOQTNLPLFTHSSAAMDPTTLEQLCTGLQOQDLHLDTCRGVWGEEDSELGNMDEPIVTV 143
QY 120 VKKFGIYDYLOEKGYSDCAMEIYVENMRALTSTTLQKRLTKMGGLNSP 172
DB 144 VKKFGIYDYLOEKGYSDCAMEIYVENMRALTSTTLQKRLTKMGGLNSP 196

RESULT 35
ADSL6363
ID ADSL6363 standard; protein; 152 AA.
XX
AC ADSL6363;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human interferon (IFN) tau (I85L) protein #2.
XX
KM Interferon; IFN; antiviral; antineoplastic; immunomodulator;
KM IFN related disorder; autoimmune disease; multiple sclerosis;
KM diabetes mellitus; lupus erythematosus; Crohn's disease; asthma; allergy;
KM psoriasis; viral infection; hepatitis C; hepatitis B; viral encephalitis;
KM cell proliferation disease; cancer; osteosarcoma; basal cell carcinoma;
KM multiple myeloma; chronic lymphocytic leukaemia; Kaposi's sarcoma;
KM renal-cell carcinoma; ovarian cancer; hairy-cell leukaemia;
KM Hodgkin's disease; gene therapy; human; IFN tau.
XX
OS Homo sapiens.
XX
PN US2004175359-A1.
XX
PD 09-SEP-2004.
XX
PF 30-SEP-2003; 2003US-00677093.
XX
PR 12-NOV-2002; 2002US-0425851P.
XX
PA (DESSU/) DESJARLAIS J R.
PA (MARS/) MARSHALL S A.
PA (MOY/) MO Y.
PA (THOM/) THOMASON A R.
XX
PI Desjarlais JR, Marshall SA, Mo Y, Thomason AR;
XX
DR WPI; 2004-642104/62.
XX
PT Novel type 1 interferon (IFN) having antiviral, antineoplastic or
PT immunomodulatory activity same as wild-type IFN, and being circularly
PT permuted or cyclized to provide modulated characteristics, useful for
PT treating IFN related diseases.
XX
PS Disclosure; SEQ ID NO 54; 48bp; English.
XX
CC The present invention relates to a type 1 interferon (IFN) comprising
CC antiviral, antineoplastic and immunomodulatory activity similar to a
CC naturally occurring IFN and has been circularly permuted or cyclised and
CC has at least one modulated characteristic as compared to the naturally
CC occurring IFN. The invention is useful for treating IFN related disorder
CC which includes autoimmune diseases such as multiple sclerosis, diabetes
CC mellitus, lupus erythematosus, Crohn's disease, asthma, allergies and
CC psoriasis, viral infections such as hepatitis C, hepatitis B and viral
CC osteosarcoma, basal cell carcinoma, multiple myeloma, chronic lymphocytic
CC leukaemia, Kaposi's sarcoma, renal-cell carcinoma, ovarian cancer, hairy-
CC cell leukaemia and Hodgkin's disease. The invention is also useful in
CC gene therapy. The present sequence is human interferon (IFN) protein.
XX
SQ Sequence 152 AA;

```

```

QY 1 CYLSRKMLDARENIKLLDRNMRSLPSHCLQDRKDFGLPQEWKESDQLQKQAPFVLVEM 60
DB 1 CYLSRKMLDARENIKLLDRNMRSLPSHCLQDRKDFGLPQEWKESDQLQKQAPFVLVEM 60
QY 61 LOOSFNLFTYTHSSAAMDPTTLEQLCTGLQOQDLHLDTCRGVWGEEDSELGNMDEPIVTV 120
DB 61 LOOSFNLFTYTHSSAAMDPTTLEQLCTGLQOQDLHLDTCRGVWGEEDSELGNMDEPIVTV 108
QY 121 KKYFGIYDYLOEKGYSDCAMEIYVENMRALTSTTLQKRLTK 164
DB 109 KKYFGIYDYLOEKGYSDCAMEIYVENMRALTSTTLQKRLTK 152

RESULT 36
AAB49783
ID AAB49783 standard; protein; 195 AA.
XX
AC AAB49783;
XX
DT 23-APR-2001 (first entry)
XX
DE Bovine TP-1 amino acid sequence.
XX
KM Human; keratinocyte derived interferon; KDI; viral infection; lymphoma;
KM immune system related disorder; cancer; multiple sclerosis; AIDS;
KM hepatitis; Cryptosporidium parvum infection; leukaemia; arthritis;
KM diabetes; allergy; chronic myelogenous leukaemia.
XX
OS Bos sp.
XX
PN WO200107608-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JAN-2000; 2000WO-US001239.
XX
PR 21-JUL-1999; 99US-00358587.
PR 21-JUL-1999; 99WO-US016424.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Moore PA, Lafleur DW;
XX
DR WPI; 2001-138557/14.
XX
PT Isolated keratinocyte derived interferon protein and polynucleotide used
PT to prevent, treat or ameliorate an immune system-related disorder, viral
PT infection, viral exposure and cancer.
XX
PS Disclosure; Fig 4; 303pp; English.
XX
CC This invention relates to human polynucleotide sequence AAF72333 which
CC encodes keratinocyte derived interferon (KDI) protein AAB49774, which is
CC a member of the interferon family. AAF72338 represents the codon
CC optimized sequence of KDI. The human KDI gene is located on chromosome 9.
CC The specification includes KDI related protein sequences AAB49775 -
CC AAB49789. Also given in the specification are primer, probe and
CC polynucleotide sequences represented by AAF72334-AAF72370 (excluding
CC AAF72338) which are used in the isolation and characterisation of the KDI
CC sequence of the invention. The KDI polypeptide and characterisation of the KDI
CC infections and the protein and polynucleotide may be used to treat viral
CC treat or ameliorate a medical condition such as immune system-related
CC disorder, viral infection, viral exposure and cancer in a mammal.
CC Specific disorders which can be treated by KDI include multiple
CC sclerosis, lymphoma, acquired immune deficiency syndrome, viral
CC hepatitis, Cryptosporidium parvum infection, chronic myelogenous
CC leukaemia, arthritis, diabetes and allergies
XX
SQ Sequence 195 AA;

```

Query Match 86.7%; Score 786; DB 8; Length 152;
 Best Local Similarity 92.7%; Pred. No. 2,9e-79;
 Matches 152; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Query Match 79.7%; Score 723; DB 4; Length 195;
 Best Local Similarity 80.7%; Pred. No. 4.4e-72;

```
Matches 138; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
QY 1 CYLSRKMLDARENUKILDRMNRISPHSCLODRKDFGLPQEMVSGDQLQKQAPVLYEM 60
D 24 CYLSBEDHMLGARENRLRLARNRRLSPHPCLODRKDFGLPQEMVSGDQLQKQAPVLYEM 83
QY 61 LQGSFNLFYTHSSAAMDPTTLLEOLCTGLQOQLEDLDTCRGQVNGEEDSELGNDPIYTV 120
D 84 LQGSFNLFYTHSSAAMDPTTLLEOLCTGLQOQLEDLDTCLPVGGEKSDMGKGPILTV 143
QY 121 KKYFGIYDVLYQEKGYSDCAMEIVREMMRALTVSTTLQKRLTKMGDGLNS 171
D 144 KKYFGIHYVLKEXEYSDCAMEIIRMEMMRALSSSTTLQKRLTKMGDGLNS 194

RESULT 37
ABB08641
ID ABB08641 standard; protein; 195 AA.
XX
AC ABB08641;
XX
XX 25-APR-2002 (first entry)
XX
DE Bovine interferon tau SEQ ID NO 10.
XX
KM Bovine; interferon; tau; IFN; antiviral; antitumor.
XX
OS Bos taurus.
XX
PN JP2001342199-A.
XX
PD 11-DEC-2001.
XX
PE 29-MAR-2001; 2001JP-00096242.
XX
PR 30-MAR-2000; 2000JP-00093383.
XX
PR (NORO ) NORISUTSANSO KACHIKU EISEI.
PA (DAUC ) DAIICHI PHARM CO LTD.
PA (KATA ) KATAKURA IND CO LTD.
XX
XX WPI; 2002-145115/19.
DR N-PSDB; ABA97931.
XX
PT Preparation of purified interferon, for use in antiviral and antitumor
PT agents; from recombinant baculovirus containing the interferon gene.
XX
PS Disclosure; Page 11-12; 13pp; Japanese.
XX
CC The invention relates to preparation of purified interferon (IFN) in
CC which a raw material containing IFN, prepared by infecting a recombinant
CC baculovirus with a gene encoding IFN protein, is subjected to a treatment
CC including silica gel chromatography, anion exchange column chromatography
CC and metal chelate column chromatography. IFN is used as an active
CC component in antiviral agents and antitumor agents. The present sequence
CC is that of bovine interferon-tau
XX
SQ Sequence 195 AA;
Query Match 79.7%; Score 723; DB 5; Length 195;
Best Local Similarity 80.7%; Pred. No. 4.4e-72;
Matches 138; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
```

```
D 144 KKYFGIHYVLKEXEYSDCAMEIIRMEMMRALSSSTTLQKRLTKMGDGLNS 194

RESULT 38
ADP94975
ID ADP94975 standard; protein; 195 AA.
XX
AC ADP94975;
XX
DE 26-FEB-2004 (first entry)
XX
DE Bovine IFN homologue, TP-1, SEQ ID:11.
XX
KM Human keratinocyte derived interferon; human KDI; agonist; antagonist;
KM finding partner identification; immune-related disorder; cancer;
KM viral infection; viral exposure; immunomodulator; virucide; cytostatic;
KM gene therapy; TP-1; bovine; cow.
XX
OS Bos taurus.
XX
PN WO2003031566-A2.
XX
PD 17-APR-2003.
XX
PF 19-JUL-2002; 2002WO-US023214.
XX
PR 20-JUL-2001; 2001US-00908594.
PR 06-DEC-2001; 2001US-0336165P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Lafleur DW, Moore PA, Ruben SM;
XX
XX WPI; 2003-381702/36.
XX
XX
XX New isolated keratinocyte derived interferon (KDI) polypeptide, useful
XX for preventing, treating or ameliorating a medical condition, such as an
XX immune-related disorder, a viral infection, a viral exposure or cancer.
XX
XX Disclosure; SEQ ID NO 11; 398pp; English.
XX
XX The invention relates to human keratinocyte derived interferon (KDI;
XX ADP94966) and nucleic acids encoding it (ADP94965). The KDI gene is
XX located on chromosome 9q22. The invention also relates to sequences at
XX least 70% identical to the KDI nucleic acid and protein sequences; a
XX polypeptide comprising an epitope-bearing portion of KDI; recombinant
XX vectors and host cells comprising a KDI protein; a KDI-specific antibody;
XX KDI agonists and antagonists; use of KDI nucleic acids or proteins for
XX treating medical conditions; a method for the diagnosis of a pathological
XX condition or susceptibility to a pathological condition; and methods of
XX screening for KDI binding partners. The KDI polypeptides and
XX polynucleotides, and methods of the invention are useful for preventing,
XX treating or ameliorating a medical condition, such as an immune-related
XX disorder, cancer, or a viral infection or viral exposure. The present
XX sequence is related to the invention.
XX
SQ Sequence 195 AA;
Query Match 79.7%; Score 723; DB 7; Length 195;
Best Local Similarity 80.7%; Pred. No. 4.4e-72;
Matches 138; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
```

Db 144 KKYFGIHHVYLKEKESDCAWEIIRMEMMRALSSSTTLQKRLRMGGDLNS 194

RESULT 39
AAW04539 standard; protein; 195 AA.

XX AAR04539;
XX
AC AAR04539;
XX
XX 25-MAR-2003 (revised)
DT 17-SEP-1990 (first entry)
XX
XX cDNA clone of sequence encoding bovine trophoblast protein-1 (bTP-1).
DE
XX Bovine trophoblast protein-1; bTP-1; fertility; da.
KM
XX Sue acrofa.
OS
XX EP367063-A.
PN
XX 09-MAY-1990.
PD
XX
XX 23-OCT-1989; 89EP-00119642.
PF
XX 26-OCT-1988; 88US-00262870.
PR
XX (UMOR) UNIV MISSOURI.
PA
XX
XX Roberts MR, Imakawa K;
PI
XX WPI; 1990-141062/19.
DR
XX N-PSDB; AAQ04285.
XX
XX PT Recombinant bovine trophoblast protein-1 - used for enhancing fertility
or treating viral diseases in mammal, esp. cattle.
XX
XX PS Claim 3; Fig 1; 27pp; English.
XX
XX The bTP-1 produced from the gene may be used to promote fertility or
CC treat viral disease in cattle. The gene may also be used to provide
CC transgenic animals with enhanced fertility, or in prophylactic and
CC therapeutic treatment of other mammals. (Updated on 25-MAR-2003 to
CC correct PA field.)
CC
XX
SQ Sequence 195 AA;

Query Match 79.4%; Score 720; DB 2; Length 195;
Best Local Similarity 80.7%; Pred. No. 9.5e-72;
Matches 138; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVEGDLQKQDAFPVLYEM 60
Db 24 CYLSEDHNLGARENLRLARNRRLSPHPCLODRKDFGLPQEMVEGDLQKQDAISVLHEM 83
Oy 61 LQGSFNLFYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
Db 84 LQOCLNLFYTEHSSAAMWTTLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 143
Oy 121 KKYFGIYDYLQEKGYSDCAWEIYRVEMMRALVTSTLQKRLTMGGDLNS 171
Db 144 KKYFGIHHVYLKEKESDCAWEIIRMEMMRALSSSTTLQKRLRMGGDLNS 194

RESULT 40
AAW70809 standard; protein; 173 AA.

XX AAM70809;
XX
XX 04-FEB-1999 (first entry)
DT
XX
XX A tau modified interferon protein oh-IFN-tau-d3.
DE
XX

KM Tau modified interferon protein; oh-IFN-tau-d3; antiviral activity;
KM Interferon activity; antitumor; autoimmune disease.
XX
XX OS Unidentified.
XX
XX JP10295382-A.
PN
XX 10-NOV-1998.
PD
XX
XX 24-APR-1997; 97JP-00106941.
PF
XX 24-APR-1997; 97JP-00106941.
PR
XX (SANY) SANKYO CO LTD.
PA
XX WPI; 1999-038279/04.
DR
XX N-PSDB; AAV70626.
DR
XX
XX PT An interferon tau modified body - used as e.g. an antiviral agent.
XX
XX PS Claim 2; Page 14; 29pp; Japanese.
XX
XX The present sequence represents a tau modified interferon protein
CC designated oh-IFN-tau-d3. The interferon tau modified protein has a high
CC antiviral activity and is low in cytotoxicity. The protein has interferon
CC activity, and can be used as an antiviral agent, an antitumor agent, or
CC treating an autoimmune disease.
CC
XX
SQ Sequence 173 AA;

Query Match 76.2%; Score 691; DB 2; Length 173;
Best Local Similarity 76.2%; Pred. No. 1.4e-68;
Matches 131; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVEGDLQKQDAFPVLYEM 60
Db 2 CYLSERMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVEGDLQKQDAISVLHEM 61
Oy 61 LQGSFNLFYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
Db 62 LQGSFNLFYTEHSSAANDTTLLEQLCTGLHQQLDNLDAICGQVNGEEDSALGRTPVTLAL 121
Oy 121 KKYFGIYDYLQEKGYSDCAWEIYRVEMMRALVTSTLQKRLTMGGDLNSP 172
Db 122 KKYFGIHHVYLKEKESDCAWEIYRVEMMRALVTSTLQKRLTMGGDLNSP 173

RESULT 41
ADG42697 standard; protein; 171 AA.

XX ADG42697;
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Human interferon tau-1 precursor.
DE
XX
XX Human; NOVX; GAGE-like protein; interferon; GPCR; mast cell protease;
KM hepatocyte nuclear factor; cancer; immune disorder; hepatic disorder;
KM trunna; HIV; Parkinson's disease; Alzheimer's disease.
XX
XX Homo sapiens.
OS
XX
XX US2003202971-A1.
PN
XX 30-OCT-2003.
PD
XX
XX 06-MAY-2002; 2002US-00139854.
PF
XX 15-FEB-2000; 2000US-0182723P.
PR 15-FEB-2000; 2000US-0182724P.
PR 15-FEB-2000; 2000US-0182733P.
PR 22-FEB-2000; 2000US-0183896P.

PR 23-FEB-2000; 2000US-0184275P.
 PR 23-FEB-2000; 2000US-0184482P.
 PR 23-FEB-2000; 2000US-0184497P.
 PR 24-FEB-2000; 2000US-0184744P.
 PR 13-APR-2000; 2000US-0197083P.
 PR 10-AUG-2000; 2000US-0224157P.
 PR 18-SEP-2000; 2000US-0233405P.
 PR 27-SEP-2000; 2000US-0236060P.
 PR 02-JAN-2001; 2001US-0259414P.
 PR 18-JAN-2001; 2001US-0262454P.
 PR 14-FEB-2001; 2001US-00783429.
 XX
 PA (MAJU/) MAJUMDER K.
 XX
 PI Majumder K;
 XX
 DR WPI; 2003-900615/82.
 XX
 PT Novel isolated NOVX polypeptide useful for treating cancer, immune
 XX disorders, hepatic disorders, AIDS, Parkinson's disease.
 PS
 XX Disclosure; SEQ ID NO 58; 155pp; English.
 CC The invention relates to an isolated NOVX polypeptide comprising mature
 CC form of protein having a fully defined sequence ADG42655ADG42659, NOV8
 CC and NOV10, a variant of mature form of the protein, where any amino acid
 CC in mature protein changed to a different amino acid, provided that not
 CC more than 50% of amino acid in sequence of mature protein are so changed,
 CC or its fragment. Also included are an isolated nucleic acid molecule (NA)
 CC encoding NOVX (or portion or variant), a vector comprising NOVX NA, a
 CC cell comprising the vector, an anti-NOVX antibody, determining (M1) the
 CC presence or amount of NOVX NA in a sample, a pharmaceutical composition
 CC (comprising NOVX, NOVX NA or the antibody and carrier) and a kit
 CC comprising in one or more containers, NOV8 and NOV10 are 2 of 13
 CC disclosed NOVX proteins showing homology to GAGE (G-antigen) proteins
 CC (NOV1-4), interferons (NOV8 and 6), G protein-coupled receptors (NOV7),
 CC Mast cell proteases (NOV8 and NOV10-13) and hepatocyte nuclear factors
 CC (NOV9). The antibody is useful for determining the presence or amount of
 CC NOVX in a sample. NOVX is useful for identifying an agent that binds to
 CC NOVX and for identifying a potential therapeutic agent for use in
 CC treatment of a pathology, where the pathology use related to aberrant
 CC expression or aberrant physiological interaction of NOVX. NOVX, NOVX NA
 CC or the antibody is useful for treating or preventing a pathology
 CC associated with NOVX e.g. cancer, immune disorder, hepatic disorder,
 CC trauma, HIV, Parkinson's disease, and Alzheimer's disease. The present
 CC sequence represents a protein showing sequence similarity to a NOVX
 CC protein (or fragment).
 CC
 XX
 SQ Sequence 171 AA;
 Query March 71.6%; Score 649; DB 7; Length 171;
 Best Local Similarity 80.9%; Pred. No. 6.7e-64;
 Matches 123; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENLKILDRMNRLLSPHSCLQDRKDFGPOEMVEGSDQLQKQDAFPVLYEM 60
 Db 20 CYLSEDHMLGARENRLRLARNRLLSPHPCLODRKDFGPOEMVEGSDQLQKQDAFPVLYEM 79
 QY 61 LQGSFNLFTYTHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRQOVNGEEDSELGNDPIYTV 120
 Db 80 LQGFNLFTYTHSSAAMWTLLLEQLCTGLQOQLDHLDTCRQOVNGEEDSELGNDPIYTV 139
 QY 121 KKYFOGIDYLOEGYSDCAMEIVVENMRAL 152
 Db 140 KKYFOGIDYLOEGYSDCAMEIVVENMRAL 171
 RESULT 42
 ADJ55766
 ID ADJ55766 standard; peptide; 171 AA.
 XX
 AC ADJ55766;
 XX

DT 06-MAY-2004 (first entry)
 XX
 DE Peptide homologous to a fragment of a human NOV5 protein Segid 58.
 XX
 KW human; NOVX; neurogenesis; cell differentiation; cell motility;
 KW cell proliferation; hematopoiesis; angiogenesis; proliferative disorder;
 KW cancer; mastocytosis; immune disorder; hepatic disorder; cirrhosis;
 KW viral infection; AIDS; hepatitis; neuro-olfactory; trauma; surgery;
 KW neoplastic; adenocarcinoma; lymphoma; asthma; Crohn's disease;
 KW multiple sclerosis; Albright hereditary osteodystrophy; cytostatic;
 KW immunosuppressive; hepatotropic; virucide; anti-HIV; antiinflammatory;
 KW vulnerability; antiallthmatic; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 FN US2003199465-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 22-APR-2002; 2002US-00131409.
 XX
 PR 15-FEB-2000; 2000US-0182723P.
 PR 15-FEB-2000; 2000US-0182724P.
 PR 15-FEB-2000; 2000US-0182733P.
 PR 22-FEB-2000; 2000US-0183896P.
 PR 23-FEB-2000; 2000US-0184275P.
 PR 23-FEB-2000; 2000US-0184482P.
 PR 23-FEB-2000; 2000US-0184497P.
 PR 24-FEB-2000; 2000US-0184744P.
 PR 13-APR-2000; 2000US-0197083P.
 PR 03-JUL-2000; 2000US-0215855P.
 PR 10-AUG-2000; 2000US-0224157P.
 PR 18-SEP-2000; 2000US-0233405P.
 PR 27-SEP-2000; 2000US-0236060P.
 PR 02-JAN-2001; 2001US-0259414P.
 PR 18-JAN-2001; 2001US-0262454P.
 PR 14-FEB-2001; 2001US-00783429.
 PR 03-JUL-2001; 2001US-00898953.
 XX
 PA (MALY/) MALYANKAR U M.
 PA (TCHE/) TCHEKNEV V T.
 PA (PADI/) PADIGARU M.
 PA (TAUP/) TAUPIER R J.
 PA (SPYT/) SPYTEK K A.
 PA (GHOX/) GHO X.
 PA (SPAD/) SPADERNA S K.
 PA (BOLD/) BOLDG F L.
 PA (GERL/) GERLACH V.
 PA (ELLER/) ELLERMAN K.
 PA (MACIT/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 XX
 XX Maljankar UM, Tchernev VT, Padigaru M, Taupier RJ, Spytek KA;
 PI Guo X, Spaderma SK, Boldog FL, Gerlach V, Ellerman K, Macdougall JR;
 PI Smithson G;
 XX
 DR WPI; 2003-900202/82.
 XX
 FT New polypeptides useful for treating e.g. cancer and mastocytosis, immune
 XX disorders, hepatic disorders, viral infections, asthma.
 PT
 XX
 PS Disclosure; SEQ ID NO 58; 86pp; English.
 XX
 CC This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human NOVX proteins, as well as methods to identify small molecules that
 CC can be used to modulate or inhibit various processes including
 CC neurogenesis, cell differentiation, cell motility, cell proliferation,
 CC haematopoiesis and angiogenesis. Furthermore, they can be used in the

CC manufacture of medicaments to treat proliferative disorders (e.g. cancer
CC and metastasis), immune disorders, hepatic disorders (e.g. cirrhosis),
CC viral infections (e.g. AIDS and hepatitis), disorders of the neuro-
CC olfactory system (e.g. trauma, surgery and/or neoplastic disorders),
CC adenocarcinoma, lymphoma, asthma, Crohn's disease, multiple sclerosis and
CC also for treating Abright osteodysplasia. Accordingly, they
CC exhibit cytotoxic, immunosuppressive, hepatotropic, virucide, anti-HIV,
CC antiinflammatory, antiviral, antidiabetic and neuroprotective
CC activities. This peptide is homologous to a fragment of a human NOVX
CC protein of the invention.
XX
SQ Sequence 171 AA;
Query Match 71.6%; Score 649; DB 7; Length 171;
Best Local Similarity 80.9%; Pred. No. 6.7e-64;
Matches 123; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
QY 1 CYLSRKLMDARENILKLDNRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 60
DB 20 CYLSEDMHGLARENILRLARNRRLSPHSCLODRKDFGLPQEMVEGNGQLQKQALSVLHEM 79
QY 61 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVNGEBSDELGNDDPIYTV 120
DB 80 LQGFNLFTYTHSSAAMNTLLEQLCTGLQOQLDHLDTCLGPMVNGEKSDMGKGPILTV 139
QY 121 KKYFGIYDYLOEKGYSDCAWEIVREMMRL 152
DB 140 KKYFGIHYLYKEKYSDCAMEIIRVEMRL 171
RESULT 43
ADM76604
ID ADM76604 standard; protein, 171 AA.
XX
AC ADM76604;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human NOVX protein-related protein fragment SegID58.
XX
XX NOVX; cytotoxic; immunosuppressive; virucide; anti-HIV; hepatotropic;
KM antiinflammatory; neuroprotective; nootropic; antiparkinsonian;
KM gene therapy; vaccine; NOVX-associated disorder; cancer; immune disorder;
KM viral infection; AIDS; hepatitis; neurological disorder;
KM Alzheimer's disease; Parkinson's disease; olfactory disorder;
KM chromosome mapping; tissue typing; NOVX; human.
XX
OS Homo sapiens.
XX
PN WO2004009634-A2.
XX
PD 29-JAN-2004.
XX
PF 04-OCT-2001; 2001WO-US031284.
XX
PR 04-OCT-2000; 2000US-02378662P.
PR 02-JAN-2001; 2001US-0259414P.
PR 18-JAN-2001; 2001US-0262454P.
PR 14-FEB-2001; 2001US-00783429.
PR 03-JUL-2001; 2001US-00898953.
PR 03-OCT-2001; 2001US-00970607.
XX
PA (CURA-) CURAGEN CORP.
PI Gerlach VL, Ellerman K, MacDougall JR, Smithson G, Shimkete RA;
PI Raetelli L, Herrmann J;
XX
XX WPI; 2004-143267/14.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for diagnosing,
PT preventing or treating NOVX-associated disorders (e.g. cancer, AIDS or
PT Alzheimer's disease), and in chromosome mapping, tissue typing or
PT pharmacogenetics.

XX
PS Disclosure; SEQ ID NO 58; 173pp; English.
XX
XX This invention relates to novel NOVX polypeptides and the DNA sequences
XX which encode them. The invention may be useful for the development of
XX compounds with a cytotoxic, immunosuppressive, virucide, anti-HIV,
XX hepatotropic, antiinflammatory, neuroprotective, nootropic or
XX antiparkinsonian activity. In addition, the disclosed sequences may be
XX useful for gene therapy or development of a vaccine. The NOVX
XX polypeptide, nucleic acid or antibody is useful in the manufacture of a
XX medicament for treating or preventing NOVX-associated disorders
XX such as cancer, immune disorders, viral infections (for example AIDS or
XX hepatitis), neurological disorders (for example Alzheimer's disease or
XX Parkinson's disease) or olfactory disorders. The nucleic acids are
XX further used as hybridisation probes, in chromosome mapping, tissue
XX typing, preventive medicine, and pharmacogenetics. The present sequence
XX is that of a human protein fragment which was used to demonstrate
XX homology between the NOVX proteins of the invention and other human
XX proteins.
XX
SQ Sequence 171 AA;
Query Match 71.6%; Score 649; DB 8; Length 171;
Best Local Similarity 80.9%; Pred. No. 6.7e-64;
Matches 123; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
QY 1 CYLSRKLMDARENILKLDNRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 60
DB 20 CYLSEDMHGLARENILRLARNRRLSPHSCLODRKDFGLPQEMVEGNGQLQKQALSVLHEM 79
QY 61 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVNGEBSDELGNDDPIYTV 120
DB 80 LQGFNLFTYTHSSAAMNTLLEQLCTGLQOQLDHLDTCLGPMVNGEKSDMGKGPILTV 139
QY 121 KKYFGIYDYLOEKGYSDCAWEIVREMMRL 152
DB 140 KKYFGIHYLYKEKYSDCAMEIIRVEMRL 171
RESULT 44
AAW70808
ID AAW70808 standard; protein, 173 AA.
XX
AC AAW70808;
XX
DT 04-FEB-1999 (first entry)
XX
DE A tau modified interferon protein oh-IFN-tau-d2.
XX
XX Tau modified interferon protein; oh-IFN-tau-d2; antiviral activity;
KM interferon activity; antitumor; autoimmune disease.
XX
XX Unidentified.
XX
PN JP10295382-A.
XX
PD 10-NOV-1998.
XX
PF 24-APR-1997; 97JP-00106941.
XX
PR 24-APR-1997; 97JP-00106941.
XX
PA (SANY) SANKYO CO LTD.
PI WPI; 1999-038279/04.
XX
XX N-PSDB; AAW70625.
XX
XX An interferon tau modified body - used as e.g. an antiviral agent.
PT Claim 1; Page 13; 29pp; Japanese.
XX
XX The present sequence represents a tau modified interferon protein


```
RESULT 47
AAW56433
ID AAW56433 standard; protein; 173 AA.
XX
XX AAW56433;
XX
DT 03-AUG-1998 (first entry)
XX
XX Amino acid sequence of an interferon-tau variant protein.
DE
XX
XX Human; interferon-tau; hIFN-tau; variant; treatment; prevention;
KW viral infection; tumour; autoimmune disease.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Protein 2..173
FT /note= "mature protein"
FT Misc-difference 28 /note= "His encoded by CAC"
FT Misc-difference 59 /note= "His encoded by CAC"
FT
FT
XX WO9807863-A1.
XX
XX 26-FEB-1998.
XX
XX 20-AUG-1997; 97WO-JP002879.
XX
XX 21-AUG-1996; 96JP-00219879.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Ishimura M, Nishigaki T;
XX WPI; 1998-169167/15.
XX DR N-PSDB; AAV22980.
XX
XX Polypeptides with interferon activity - for treatment and prevention of
XX PT viral infection, tumours and autoimmune diseases.
XX
XX PS Claim 4; Page 30-31; 61pp; Japanese.
XX
XX The present sequence represents a human interferon-tau (hIFN-tau)
XX CC variant. The hIFN-tau variant protein is used for the treatment and
XX CC prevention of viral infections, tumours and autoimmune diseases
XX
XX Sequence 173 AA;
SQ
Query Match 69.2%; Score 628; DB 2; Length 173;
Best Local Similarity 69.8%; Pred. No. 1.5e-61;
Matches 120; Conservative 21; Mismatches 31; Indels 0; Gaps 0;
OY 1 CYLSRKMLDARENKILDRNRRLSPHSCLODRKFGIPQEMVSGDLOKQDAFPVLYEM 60
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 2 CDLSQHNHVLVGRKNRLDDEMRRLSPHCLDRKDFALPQEMVSGDLOKQDAISVLHEM 61
DB
OY 61 LQGSFNLPTHTSSAAMDPTLLLEQLCTGLHQQDLNLCACGQVWGEEDSALGRTPTLAL 120
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 62 LQGSFNLPTHTSSAAMDPTLLLEQLCTGLHQQDLNLCACGQVWGEEDSALGRTPTLAL 121
DB
OY 121 KKYFQGIYDYLQEKGYSDCAMEIYRVEMMRALTVSTTLQKRLTYKGGDLNSP 172
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 122 KRYFQGIHVLKKEGYSDCAMEIYRVLEIMRSFSLISQERLRMMDDGLSSP 173
DB
RESULT 48
AAW70812
ID AAW70812 standard; protein; 173 AA.
XX
XX AAW70812;
XX
```

```
DT 04-FEB-1999 (first entry)
XX
XX A human interferon-tau-d1 (hIFN-tau-d1) protein.
DE
XX
XX Tau modified interferon protein; IFN-tau-d1; antiviral activity;
KW interferon activity; antitumor; autoimmune disease.
XX
XX Homo sapiens.
OS
XX
XX JP10295382-A.
XX
XX 10-NOV-1998.
XX
XX 24-APR-1997; 97JP-00106941.
XX
XX 24-APR-1997; 97JP-00106941.
XX
XX 24-APR-1997; 97JP-00106941.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX WPI; 1999-038279/04.
XX DR N-PSDB; AAV70656.
XX
XX An interferon tau modified body - used as e.g. an antiviral agent.
XX
XX Disclosure; Page 22-23; 29pp; Japanese.
XX
XX The present sequence represents human interferon-tau-d1 (hIFN-tau-d1).
XX CC The protein is used in the course of the invention to create interferon
XX CC tau modified proteins which have a high antiviral activity and are low in
XX CC cytotoxicity. The protein has interferon activity, and can be used as an
XX CC antiviral agent, an antitumor agent, or treating an autoimmune disease
XX
XX Sequence 173 AA;
SQ
Query Match 69.2%; Score 628; DB 2; Length 173;
Best Local Similarity 69.8%; Pred. No. 1.5e-61;
Matches 120; Conservative 21; Mismatches 31; Indels 0; Gaps 0;
OY 1 CYLSRKMLDARENKILDRNRRLSPHSCLODRKFGIPQEMVSGDLOKQDAFPVLYEM 60
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 2 CDLSQHNHVLVGRKNRLDDEMRRLSPHCLDRKDFALPQEMVSGDLOKQDAISVLHEM 61
DB
OY 61 LQGSFNLPTHTSSAAMDPTLLLEQLCTGLHQQDLNLCACGQVWGEEDSALGRTPTLAL 120
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 62 LQGSFNLPTHTSSAAMDPTLLLEQLCTGLHQQDLNLCACGQVWGEEDSALGRTPTLAL 121
DB
OY 121 KKYFQGIYDYLQEKGYSDCAMEIYRVEMMRALTVSTTLQKRLTYKGGDLNSP 172
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 122 KRYFQGIHVLKKEGYSDCAMEIYRVLEIMRSFSLISQERLRMMDDGLSSP 173
DB
RESULT 49
AAW56434
ID AAW56434 standard; protein; 173 AA.
XX
XX AAW56434;
XX
DT 03-AUG-1998 (first entry)
XX
XX Amino acid sequence of an interferon-tau variant protein.
DE
XX
XX Human; interferon-tau; hIFN-tau; variant; treatment; prevention;
KW viral infection; tumour; autoimmune disease.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Protein 2..173
FT /note= "mature protein"
FT Misc-difference 28 /note= "His encoded by CAC"
FT Misc-difference 59 /note= "His encoded by CAC"
FT
```

XX WO9807863-A1.
 XX
 XX 26-FEB-1998.
 PD
 XX 20-AUG-1997; 97WO-JP002879.
 PF
 XX 21-AUG-1996; 96JP-0021879.
 PR
 XX
 XX (SANY) SANKYO CO LTD.
 PA
 XX
 XX Ieshimura M, Nishigaki T;
 PI
 XX
 XX MPI; 1998-169167/15.
 DR
 XX N-PSDB; AAV22981.
 DR
 XX
 XX Polypeptides with interferon activity - for treatment and prevention of
 PT viral infection, tumours and autoimmune diseases.
 PT
 XX
 XX Claim 5; Page 33-34; 61pp; Japanese.
 PS
 XX
 XX The present sequence represents a human interferon-tau (hIFN-tau)
 CC variant. The hIFN-tau variant protein is used for the treatment and
 CC prevention of viral infections, tumours and autoimmune diseases
 XX
 XX Sequence 173 AA;
 XQ

Query Match	69.1%	Score 627	DB 2	Length 173
Best Local Similarity	69.8%	Pred. No. 2e-61		
Matches 120; Conservative	21	Mismatches	31	Indels 0
		Gaps		0

[illegible]

RESULT 50

ID AAW70813 standard; protein; 173 AA.

AC AAW70813;

DT 04-FEB-1999 (first entry)

DE A human interferon-tau-d2 (hIFN-tau-d2) protein.

KM Tau modified interferon protein; IFN-tau-d2; antiviral activity;
KM interferon activity; antitumor; autoimmune disease.

OS Homo sapiens.

PN JP10295382-A.

PD 10-NOV-1998.

PF 24-APR-1997; 97JP-00106941.

PR 24-APR-1997; 97JP-00106941.

PA (SANY) SANKYO CO LTD.

DR WPI; 1999-038279/04.

XX

xx Disclosure; Page 24-25; 29pp; Japanese.
 ps
 xx The present sequence represents human interferon-tau-d2 (hIFN-tau-d2).
 cc The protein is used in the course of the invention to create interferon
 cc tau modified proteins which have a high antiviral activity and are low in
 cc cytotoxicity. The protein has interferon activity, and can be used as an
 cc antiviral agent, an antitumor agent, or treating an autoimmune disease
 cc
 xx Sequence 173 AA;
 sq

Query Match	69.1%	Score 627	DB 2	Length 173
Best Local Similarity	69.8%	Pred. No. 2e-61		
Matches 120; Conservative	21	Mismatches	0	Gaps 0

```
QY 1 CYLSKMLLDARENKLLDPMNRSLSPHSCTGDRKPGLEQOEWEQGLQKDKAPVLYEM 60
QY 2 CDLSGYHVLVGRKNRLRLDEMRRSLPHFLCGRKPPALQOEWEQGLQEAQALSVLHEM 61
Db 2 CDLSGYHVLVGRKNRLRLDEMRRSLPHFLCGRKPPALQOEWEQGLQEAQALSVLHEM 61
QY 61 LQGSNLFYTERHSSAAMDPTLLLEQLCTGICQQLDHLPTRCQVMEGSEDSLGMDFVTV 120
Db 61 LQGSNLFYTERHSSAAMDPTLLLEQLCTGICQQLDHLPTRCQVMEGSEDSLGMDFVTV 120
QY 62 LQGSNLFYTERHSSAAMDPTLLLEQLCTGICQQLDHLPTRCQVMEGSEDSLGMDFVTV 120
Db 62 LQGSNLFYTERHSSAAMDPTLLLEQLCTGICQQLDHLPTRCQVMEGSEDSLGMDFVTV 120
QY 121 KRYFGIYDYLQEKGYSDCAMEIVEVENMRALTVSTLLQRLTKMGDINSPL 172
Db 121 KRYFGIYDYLQEKGYSDCAMEIVEVENMRALTVSTLLQRLTKMGDINSPL 172
QY 122 KRYFGIHYVLYKEKGYSDCAMEVTLEIMRSPSSLSLSOERLRIMDGDJSSP 173
Db 122 KRYFGIHYVLYKEKGYSDCAMEVTLEIMRSPSSLSLSOERLRIMDGDJSSP 173
```

Search completed: October 5, 2005, 10:34:35
Job time : 181 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 10:23:15 ; Search time 41 Seconds

(without alignments)
403.641 Million cell updates/sec

Title: US-10-694-247-2

Perfect score: 907
Sequence: 1 CYLSRKLMDARENLKULDR.....TVSTTLQKRLTKMGDLNSP 172Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79:.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	897	98.9	195	2 JS0204	ctrophoblast interf
2	880	97.0	195	2 I47068	ctrophoblast protei
3	868	95.7	195	2 I47066	ctrophoblast protei
4	865	95.4	195	2 I47069	ctrophoblast protei
5	847	93.4	172	2 A61578	ctrophoblast protei
6	846	93.3	195	2 I46272	ctrophoblast interf
7	842	92.8	195	2 A61455	ctrophoblast protei
8	806	88.9	195	2 I47067	ctrophoblast protei
9	778	85.8	195	2 I47097	ctrophoblast protei
10	745	82.1	184	2 I47098	ctrophoblast protei
11	724	79.8	195	2 A39505	ctrophoblast interf
12	723	79.7	195	2 S23751	ctrophoblast interf
13	720	79.4	195	2 A40068	ctrophoblast protei
14	720	79.4	195	2 B39505	ctrophoblast protei
15	609	67.1	195	2 A53746	interferon, tropho
16	608	67.0	195	2 A61403	interferon alpha-I
17	587	64.7	195	2 I47070	interferon alpha-I
18	585	64.5	195	2 I46397	interferon omega -
19	582	64.2	195	1 I46011	interferon alpha-I
20	513.5	56.6	190	2 S23711	interferon alpha-I
21	499	55.0	195	1 I47022	interferon alpha-I
22	497	54.8	110	2 B61578	ctrophoblast protei
23	488.5	53.9	190	2 S23712	interferon alpha-I
24	473	52.1	195	1 I47011	interferon omega-I
25	469.5	51.8	179	2 S23710	interferon alpha-I
26	454	50.1	189	2 I51970	interferon precurs
27	446	49.2	176	2 I56314	interferon-alpha -
28	444	49.0	195	1 I47021	interferon alpha-I
29	440	48.5	189	1 I47014	interferon alpha-I

30	440	48.5	189	1 I47017	interferon alpha-5
31	438	48.3	189	1 I47019	interferon alpha-1
32	431	47.5	167	2 D25843	interferon alpha-G
33	431	47.5	195	2 I46398	interferon alpha -
34	429	47.3	189	1 I47048	interferon alpha-I
35	429	47.3	189	1 I47045	interferon alpha-5
36	428	47.2	189	1 I47041	interferon alpha-1
37	427	47.1	195	2 I46975	interferon-omega20
38	426	47.0	195	2 I46972	interferon-omega44
39	425	46.9	189	2 I52347	interferon alpha-M
40	424	46.7	195	2 I46974	interferon-omega45
41	423	46.6	195	2 S70011	interferon type I
42	421	46.4	181	2 I56313	interferon alpha 2
43	421	46.4	189	2 I84454	interferon-alpha-F
44	419	46.2	167	2 E25843	interferon alpha-F
45	419	46.2	189	1 I47048	interferon alpha-I
46	408	45.0	184	1 I47042	interferon alpha-I
47	405	44.7	167	2 F25843	interferon alpha-J
48	405	44.7	189	1 I47040	interferon alpha-7
49	404	44.5	189	2 I53102	interferon-alpha-J
50	403	44.4	184	1 I47041	interferon alpha-I
51	403	44.4	184	1 I47043	interferon alpha-I
52	403	44.4	184	1 I47044	interferon alpha-I
53	398	43.9	189	1 I47016	interferon alpha-I
54	397.5	43.8	165	2 I78570	alpha 2 interferon
55	394.5	43.5	188	1 I47042	interferon alpha-2
56	392	43.2	189	2 I37584	IFN-alpha-N-protei
57	386	42.6	189	1 I47018	interferon alpha-I
58	384	42.3	189	1 I47045	interferon alpha-I
59	384	42.3	189	2 S23709	interferon alpha-1
60	380	41.9	190	2 A24401	interferon alpha-I
61	378	41.7	189	1 I47016	interferon alpha-I
62	378	41.7	190	2 I47015	interferon alpha-B
63	377	41.6	162	2 C25843	interferon alpha-8
64	377	41.6	189	1 I47044	interferon alpha-4
65	376	41.5	189	1 I47011	interferon alpha-I
66	375	41.3	189	1 I47041	interferon alpha-I
67	374	41.2	190	2 I47072	interferon alpha-7
68	372	41.0	190	1 I47042	interferon alpha-2
69	371	40.9	192	1 I47041	interferon alpha-I
70	368	40.6	189	1 I47018	interferon alpha-I
71	364	40.1	190	2 JH0468	interferon alpha-1
72	364	40.1	190	2 I49774	alpha-interferon -
73	360	39.7	189	1 I47018	interferon alpha-I
74	355	39.1	189	1 I47041	interferon alpha-I
75	351	38.7	189	1 I47041	interferon alpha-I
76	342	37.7	189	1 I47046	interferon alpha-I
77	340.5	37.5	194	2 JS0664	interferon alpha-I
78	340	37.5	189	2 I49773	murine interferon
79	331.5	36.5	186	1 I47044	interferon alpha-I
80	318	35.1	187	2 I46206	interferon-alpha -
81	316	34.8	187	2 I46204	interferon-alpha -
82	287.5	31.7	186	1 I47042	interferon beta-2
83	257	28.3	186	1 I47041	interferon beta-I
84	255	28.1	186	1 I47043	interferon beta-3
85	253.5	27.9	187	1 I47041	interferon beta-1
86	250.5	27.6	170	2 A48772	interferon, atypic
87	230.5	25.4	186	1 I47041	interferon beta-1
88	180.5	19.9	90	2 I57395	interferon alpha-2
89	174	19.0	72	2 I79343	interferon alpha T
90	172.5	19.0	184	2 J05424	interferon beta pr
91	164	18.1	182	1 I47041	interferon beta pr
92	141	15.5	66	2 I58939	interferon alpha N
93	134.5	14.8	193	2 I50693	interferon - chick
94	133.5	14.7	191	2 S57642	interferon precurs
95	110.5	12.2	72	2 I73333	interferon alpha-2
96	110	12.1	58	2 I79344	interferon alpha O
97	107.5	11.9	72	2 I73332	interferon alpha-2
98	85	9.4	1920	2 A53188	pericentritin - mous
99	83	9.2	741	2 T48006	hypothetical prote
100	81.5	9.0	239	2 G96740	hypothetical prote
101	80.5	8.9	581	2 S63183	CNN1 protein - Yea
102	80.5	8.9	1269	2 F84730	probable myosin he

103	80	8.8	2042	2	T18339	variant-specific s
104	79.5	8.8	344	2	B80401	cofactor biosynthe
105	79.5	8.8	379	2	H82284	queuine tRNA-ribos
106	79.5	8.8	3026	2	T28431	variant surface pr
107	78	8.6	489	2	S05474	keratin 8, type II
108	78	8.6	3255	2	G81702	adherence factor T
109	77.5	8.5	1029	2	T41366	RanBP7/importin-be
110	77	8.5	576	1	B35128	DNA repair and gen
111	76.5	8.4	115	2	B71029	hypothetical prote
112	76.5	8.4	614	2	T29902	hypothetical prote
113	76.5	8.4	1131	2	AD2166	two-component sens
114	76	8.4	519	2	A89903	conserved hypot het
115	76	8.4	634	2	G81652	Arp-dependent heli
116	75	8.3	561	2	G71818	probable thiophene
117	75	8.3	4502	2	A23547	keratin, type II c
118	74.5	8.2	374	2	AG0387	queuine tRNA-ribos
119	74.5	8.2	545	2	H83079	hypothetical prote
120	74	8.2	481	2	H87282	conserved hypot het
121	74	8.2	1802	2	T00020	bacterial blight-r
122	73.5	8.1	269	2	F89455	protein F55A4.4 [i
123	73.5	8.1	478	2	U02034	RNA-directed RNA p
124	73.5	8.1	1006	2	T26770	hypothetical prote
125	73	8.0	534	2	F96713	unknown protein T6
126	73	8.0	1073	2	S14032	kinesin-related pr
127	73	8.0	1085	2	T38378	kinesin-like prote
128	73	8.0	1938	2	UC5421	smooth muscle myos
129	73	8.0	1972	2	UC5420	smooth muscle myos
130	72.5	8.0	822	2	S56801	hypothetical prote
131	72.5	8.0	980	2	T00045	cellodextrin phosp
132	72.5	8.0	1642	2	T08880	MDA receptor-bind
133	72.5	8.0	2168	2	T30171	keratin 8, type II
134	72	7.9	487	2	U04007	cytokeratin EndoA
135	72	7.9	490	2	JS0658	hypothetical prote
136	72	7.9	674	2	C81505	hypothetical prote
137	72	7.9	680	2	E72033	hypothetical prote
138	72	7.9	680	2	B86590	hypothetical prote
139	72	7.9	756	2	T05829	hypothetical prote
140	72	7.9	758	2	T32861	hypothetical prote
141	72	7.9	781	2	T05206	hypothetical prote
142	72	7.9	796	2	C85220	hypothetical prote
143	72	7.9	4589	2	T14914	dynein beta heavy
144	72	7.9	4924	2	T50176	probable peptide s
145	71.5	7.9	353	2	T05552	SREI protein-relat
146	71.5	7.9	522	2	D96764	unknown protein F2
147	71.5	7.9	559	2	B72487	hypothetical prote
148	71.5	7.9	607	2	S77092	hypothetical prote
149	71.5	7.9	658	2	T50080	probable DNA repai
150	71.5	7.9	829	2	G69729	excinuclease ABC c
151	71.5	7.9	829	2	T46556	DNA topoisomerase
152	71.5	7.9	830	2	G96900	DNA gyrase (topois
153	71.5	7.9	856	2	T58411	protein-tyrosine k
154	71.5	7.9	863	2	C88546	protein R107.4 [im
155	71.5	7.9	894	1	A41527	protein-tyrosine k
156	71.5	7.9	2023	1	T13154	polycomb protein e
157	71.5	7.9	2136	2	B84651	hypothetical prote
158	71	7.8	226	2	C90711	probable response
159	71	7.8	226	2	B64796	transcription regu
160	71	7.8	226	2	G85561	Shigella regulator
161	71	7.8	310	2	S43865	cytokeratin 8, typ
162	71	7.8	372	2	T51082	hypothetical prote
163	71	7.8	505	1	S76229	DNA repair protein
164	71	7.8	722	2	AD2222	Arp-dependent heli
165	71	7.8	757	2	D95103	X-pro dipeptidyl-p
166	71	7.8	780	2	T27941	hypothetical prote
167	71	7.8	795	2	B97971	leucine-CRNA ligas
168	71	7.8	806	2	G71805	conserved hypot het
169	71	7.8	2819	2	AG0551	hypothetical prote
170	70.5	7.8	248	2	T23708	hypothetical prote
171	70.5	7.8	415	2	H84718	conserved hypot het
172	70.5	7.8	558	2	E72220	hypothetical prote
173	70.5	7.8	656	2	S73313	excinuclease ABC (
174	70.5	7.8	660	2	C84099	preprotein translo
175	70.5	7.8	839	2	C97250	
176	70.5	7.8	863	2	S37040	paramyosin - tapew
177	70.5	7.8	892	2	A56213	DNA excision-repai
178	70.5	7.8	1039	2	F71427	hypothetical prote
179	70.5	7.8	1046	2	T29776	hypothetical prote
180	70	7.7	179	2	B83903	RNA polymerase ECF
181	70	7.7	332	2	AD2384	transposase alr462
182	70	7.7	399	2	B75201	hypothetical prote
183	70	7.7	448	2	A36311	70K uI small nucle
184	70	7.7	584	2	A97171	uncharacterized pr
185	70	7.7	609	4	A56379	ZP3 receptor precu
186	70	7.7	600	2	T22803	hypothetical prote
187	70	7.7	725	1	UC5016	hyaluronan recepto
188	70	7.7	1067	2	H75139	isolectin-CRNA gym
189	70	7.7	2677	2	A38194	desmoplakin I - hu
190	69.5	7.7	452	2	S77436	sigma factor s10G
191	69.5	7.7	610	2	A10466	ATP-dependent DNA
192	69.5	7.7	822	2	AB0238	haemin storage sys
193	69.5	7.7	822	2	T47007	hypothetical prote
194	69.5	7.7	866	2	F64625	type I restriction
195	69.5	7.7	942	2	S23251	hypothetical prote
196	69.5	7.7	1139	2	T23018	hypothetical prote
197	69.5	7.7	1707	2	AH2085	two-component relat
198	69	7.6	272	2	S16325	homeotic protein A
199	69	7.6	346	2	D90156	conserved hypot het
200	69	7.6	425	2	E64403	translation releas
201	69	7.6	483	2	A34720	keratin 8, type II
202	69	7.6	513	2	C82366	conserved hypot het
203	69	7.6	670	2	A83255	excinuclease ABC s
204	69	7.6	715	2	S77439	hypothetical prote
205	69	7.6	996	1	S42208	NAD ADP-ribosyltra
206	69	7.6	1153	2	B97718	hypothetical prote
207	69	7.6	1237	2	A31334	phosphorylase kina
208	69	7.6	1972	1	A41604	myosin heavy chain
209	68.5	7.6	153	2	B82153	hypothetical prote
210	68.5	7.6	209	2	B72247	ribosomal protein
211	68.5	7.6	367	1	A46355	site-specific DNA-
212	68.5	7.6	392	1	RRNZ6P	polymerase-aassocia
213	68.5	7.6	431	2	A48094	serum and glucocor
214	68.5	7.6	442	2	S73472	probable thiophene
215	68.5	7.6	487	2	G71432	hypothetical prote
216	68.5	7.6	504	2	A48550	hypothetical prote
217	68.5	7.6	590	2	A10174	probable lon prote
218	68.5	7.6	694	2	A53978	protein-tyrosine-p
219	68.5	7.6	795	2	S30874	hypothetical prote
220	68.5	7.6	836	2	S49940	cell division cont
221	68.5	7.6	875	2	B71850	type I restriction
222	68.5	7.6	935	2	T50774	probable translati
223	68.5	7.6	948	2	C82077	glutamate-ammonia
224	68.5	7.6	1039	2	C64418	isolencine-cRNA 11
225	68.5	7.6	1132	2	T44001	major DNA binding
226	68.5	7.6	1162	2	T30194	nuclear protein SA
227	68.5	7.6	2291	1	A46147	spectrin beta chain
228	68	7.5	244	2	H75107	hypothetical prote
229	68	7.5	316	2	A41781	proteoglycan-Ib -
230	68	7.5	325	2	S18575	svrm protein - Rhi
231	68	7.5	326	2	A45505	svrm protein - Rhi
232	68	7.5	326	2	A45505	svrm protein - Rhi
233	68	7.5	338	2	F95319	Svrm transcription
234	68	7.5	338	2	A13183	aldo/keto reductas
235	68	7.5	349	2	T38904	ATRA-binding prote
236	68	7.5	380	2	D64129	probable 8-amino-7
237	68	7.5	440	2	UC2532	secretin receptor
238	68	7.5	489	2	A47200	EcoA system protei
239	68	7.5	493	2	F86133	hypothetical prote
240	68	7.5	493	2	C91282	hypothetical prote
241	68	7.5	583	2	C84788	probable myosin he
242	68	7.5	809	2	F81312	leucine-CRNA ligas
243	68	7.5	839	1	TVHUUV	transforming prote
244	68	7.5	842	2	S56819	hypothetical prote
245	68	7.5	848	1	S64732	scaffold attachmen
246	68	7.5	908	2	T50685	sech protein limpo
247	68	7.5	994	2	T49276	c-mec tyrosine kin
248	68	7.5	1063	2	T18255	cytoskeleton assem
249	68	7.5	2139	2	T18296	myosin heavy chain

249	68	7.5	5255	2	T31677	bactitracin synthet	322	66	7.3	1181	2	C82500	ICMF-related prote
250	67.5	7.4	109	2	F75105	hypothetical prote	323	66	7.3	1289	2	I84505	calcium-dependent
251	67.5	7.4	135	2	T29473	hypothetical prote	324	66	7.3	1610	2	T11681	hypothetical prote
252	67.5	7.4	300	2	E96585	hypothetical prote	325	66	7.3	1953	2	S63244	BN11 protein - yea
253	67.5	7.4	394	2	T19181	hypothetical prote	326	66	7.3	2524	2	A35844	XorC protein - Af
254	67.5	7.4	457	2	T05651	hypothetical prote	327	65.5	7.2	206	2	A64095	ribosomal protein
255	67.5	7.4	773	2	T00554	hypothetical prote	328	65.5	7.2	252	2	F89869	conserved hypothet
256	67.5	7.4	846	2	A86663	aminopeptidase N l	329	65.5	7.2	300	2	S50727	sporulation protei
257	67.5	7.4	916	2	D81072	preproteol translo	330	65.5	7.2	351	2	A10991	cell division prot
258	67.5	7.4	1092	2	T12520	hypothetical prote	331	65.5	7.2	364	2	D90699	probable capsule a
259	67.5	7.4	1138	2	T24635	hypothetical prote	332	65.5	7.2	364	2	G85549	probable capsule a
260	67.5	7.4	1964	2	A59282	nonmuscle myosin I	333	65.5	7.2	364	2	F64781	YbbB protein - Sac
261	67.5	7.4	2147	2	T21328	hypothetical prote	334	65.5	7.2	375	2	D97268	toxic anion resist
262	67	7.4	234	1	J00506	dehiodiolcin synh	335	65.5	7.2	375	2	A80552	queine tRNA-ribos
263	67	7.4	244	2	A40625	tetrachloro-P-hydr	336	65.5	7.2	378	2	A82083	phosphonate metabo
264	67	7.4	268	2	T24253	hypothetical prote	337	65.5	7.2	387	2	T36697	hypothetical prote
265	67	7.4	293	2	F70329	hypothetical prote	338	65.5	7.2	405	2	T47595	RING finger protei
266	67	7.4	326	2	T51811	protein farnesyltr	339	65.5	7.2	430	2	B40646	foyl-polyglutamat
267	67	7.4	391	2	H90308	transposase ISCl31	340	65.5	7.2	463	2	T16503	hypothetical prote
268	67	7.4	437	2	S52014	H+-transporting tw	341	65.5	7.2	465	2	T27415	hypothetical prote
269	67	7.4	484	2	C88264	protein kin-15 (im	342	65.5	7.2	496	2	AC1306	carboxy-terminal p
270	67	7.4	488	2	I44330	protein-tyrosine k	343	65.5	7.2	566	2	F70028	transmembrane rece
271	67	7.4	501	2	G84314	replication factor	344	65.5	7.2	803	2	H87197	penicillin binding
272	67	7.4	503	2	I46015	aromatase (EC 1.14	345	65.5	7.2	846	2	JN0324	lysine aminopeptid
273	67	7.4	535	2	S74703	hypothetical prote	346	65.5	7.2	846	2	S23157	membrane alanyl am
274	67	7.4	629	2	A28666	keratin, 65K type	347	65.5	7.2	913	2	S61580	probable membrane
275	67	7.4	629	2	F86351	protein T26F17.2 (348	65.5	7.2	932	2	G86857	isoleucine-tRNA 11
276	67	7.4	798	2	S62031	vacuolar protein s	349	65.5	7.2	944	2	A10507	isoleucyl-tRNA syn
277	67	7.4	891	2	B84614	hypothetical prote	350	65.5	7.2	1013	2	T31211	tyrc protein homo
278	67	7.4	931	2	B75027	hypothetical prote	351	65.5	7.2	1015	2	AF2061	hypothetical prote
279	67	7.4	941	2	B53335	Na+/Ca++-exchangin	352	65.5	7.2	1088	2	T18559	hypothetical prote
280	67	7.4	1008	2	A82304	hypothetical prote	353	65.5	7.2	1127	2	T24404	hypothetical prote
281	67	7.4	1066	2	F71100	isoleucine-tRNA 11	354	65.5	7.2	1164	2	T03814	tumor suppressor p
282	67	7.4	1241	2	S40528	phosphorylase kina	355	65.5	7.2	1866	1	GWME2C	genome polypeptein
283	67	7.4	1278	2	B70236	hypothetical prote	356	65.5	7.2	2101	2	A42184	nuclear mitotic ap
284	67	7.4	1805	1	A64224	hypothetical prote	357	65	7.2	220	2	E75090	adenylate kinase (
285	66.5	7.3	382	2	A64057	queine tRNA-ribos	358	65	7.2	327	2	F83715	indirect positive
286	66.5	7.3	439	2	AD2555	hypothetical prote	359	65	7.2	338	2	S44261	SRI1 protein - Ara
287	66.5	7.3	494	2	T46442	hypothetical prote	360	65	7.2	370	2	A25004	keratin, 53K type
288	66.5	7.3	513	1	ZABP4	replication initia	361	65	7.2	393	2	E30272	transposase ISCl31
289	66.5	7.3	534	2	F95202	KH domain protein	362	65	7.2	362	2	C83697	transposase (01) B
290	66.5	7.3	537	2	F98069	conserved hypothet	363	65	7.2	405	2	C83781	transposase (01) B
291	66.5	7.3	562	2	S61295	heat shock protein	364	65	7.2	405	2	D83826	transposase (01) B
292	66.5	7.3	563	2	T30087	hypothetical prote	365	65	7.2	405	2	B83843	transposase (01) B
293	66.5	7.3	597	2	B53978	protein-tyrosine-p	366	65	7.2	405	2	B83891	transposase (01) B
294	66.5	7.3	608	2	B81401	hypothetical prote	367	65	7.2	405	2	B83893	transposase (01) B
295	66.5	7.3	608	2	T02299	hypothetical prote	368	65	7.2	405	2	A84042	transposase (01) B
296	66.5	7.3	760	2	A40195	meprin A (EC 3.4.2	369	65	7.2	408	2	G83745	transposase (01) B
297	66.5	7.3	876	2	I49152	protein-tyrosine k	370	65	7.2	410	2	AD2087	gas vesicle protei
298	66.5	7.3	880	1	JC4166	protein-tyrosine k	371	65	7.2	437	2	S74591	Sensory transducti
299	66.5	7.3	880	2	B53743	protein-tyrosine k	372	65	7.2	441	2	F83680	transposase (01) B
300	66.5	7.3	916	2	G81797	preproteol translo	373	65	7.2	441	2	F83683	transposase (01) B
301	66.5	7.3	1110	2	T49091	gamma response I p	374	65	7.2	441	2	B83796	transposase (01) B
302	66.5	7.3	1195	2	E96615	hypothetical prote	375	65	7.2	441	2	C83813	transposase (01) B
303	66	7.3	158	2	A12064	hypothetical prote	376	65	7.2	441	2	T44292	transposase (01) B
304	66	7.3	214	2	B64378	hypothetical prote	377	65	7.2	451	1	S75239	hypothetical prote
305	66	7.3	234	2	T52100	MADS-box transcrip	378	65	7.2	459	2	F83996	transposase (01) B
306	66	7.3	237	2	A83759	crithalose operon t	379	65	7.2	463	2	H84118	transposase (01) B
307	66	7.3	258	2	S75726	hypothetical prote	380	65	7.2	469	2	A99577	conserved hypothet
308	66	7.3	287	2	T26411	hypothetical prote	381	65	7.2	536	2	B84549	probable ubiquitin
309	66	7.3	340	2	T49006	farnesyltransferas	382	65	7.2	552	2	D82878	phosphomannomutase
310	66	7.3	375	2	E85536	tRNA-guanine trans	383	65	7.2	597	2	D87665	methyl-accepting C
311	66	7.3	375	2	C38530	queine tRNA-ribos	384	65	7.2	621	2	S10450	myosin heavy chain
312	66	7.3	375	2	A99686	cRNA-guanine trans	385	65	7.2	636	2	A45949	mezozote surfact
313	66	7.3	390	2	A60093	cyclokeratin, type	386	65	7.2	658	2	T21618	hypothetical prote
314	66	7.3	399	2	T23470	hypothetical prote	387	65	7.2	664	2	S64123	hypothetical prote
315	66	7.3	553	2	G83866	hypothetical prote	388	65	7.2	715	2	S73637	ATP-dependent prot
316	66	7.3	562	2	G70002	hypothetical prote	389	65	7.2	738	2	S35093	plakoglobin - Afri
317	66	7.3	786	2	I49274	mammary gland fact	390	65	7.2	763	2	F95125	ATP-dependent DNA
318	66	7.3	846	2	E81328	probable periplasm	391	65	7.2	763	2	C97996	hypothetical prote
319	66	7.3	853	1	S20595	glycogen phosphory	392	65	7.2	799	2	T00331	hypothetical prote
320	66	7.3	1031	1	A38713	kinesin heavy chai	393	65	7.2	881	2	AD2580	two component sens
321	66	7.3	1054	2	B38919	hypothetical prote	394	65	7.2	881	2	C97362	protein sensor pro

395	65	7.2	894	1	FAHUA2	alpha-actinin 2 -
396	65	7.2	930	2	A95193	isolectin-1C-RNA b
397	65	7.2	930	2	E98059	isolectin-1C-RNA b
398	65	7.2	941	2	S78633	isolectin-1C-RNA b
399	65	7.2	991	2	S78633	isolectin-1C-RNA b
400	65	7.2	992	2	S32902	6-phosphofructokin
401	65	7.2	1076	2	S44764	C27D11.1 protein -
402	65	7.2	1277	2	E70224	hypothetical prote
403	65	7.2	1276	2	A39401	metazoa surface
404	65	7.2	1276	2	A39401	metazoa surface
405	65	7.2	1276	2	A39401	metazoa surface
406	65	7.2	1276	2	A39401	metazoa surface
407	65	7.2	1276	2	A39401	metazoa surface
408	65	7.2	1276	2	A39401	metazoa surface
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423	65	7.2	1276	2	A39401	metazoa surface
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429	65	7.2	1276	2	A39401	metazoa surface
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431	65	7.2	1276	2	A39401	metazoa surface
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433	65	7.2	1276	2	A39401	metazoa surface
434	65	7.2	1276	2	A39401	metazoa surface
435	65	7.2	1276	2	A39401	metazoa surface
436	65	7.2	1276	2	A39401	metazoa surface
437	65	7.2	1276	2	A39401	metazoa surface
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439	65	7.2	1276	2	A39401	metazoa surface
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442	65	7.2	1276	2	A39401	metazoa surface
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445	65	7.2	1276	2	A39401	metazoa surface
446	65	7.2	1276	2	A39401	metazoa surface
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452	65	7.2	1276	2	A39401	metazoa surface
453	65	7.2	1276	2	A39401	metazoa surface
454	65	7.2	1276	2	A39401	metazoa surface
455	65	7.2	1276	2	A39401	metazoa surface
456	65	7.2	1276	2	A39401	metazoa surface
457	65	7.2	1276	2	A39401	metazoa surface
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459	65	7.2	1276	2	A39401	metazoa surface
460	65	7.2	1276	2	A39401	metazoa surface
461	65	7.2	1276	2	A39401	metazoa surface
462	65	7.2	1276	2	A39401	metazoa surface
463	65	7.2	1276	2	A39401	metazoa surface
464	65	7.2	1276	2	A39401	metazoa surface
465	65	7.2	1276	2	A39401	metazoa surface
466	65	7.2	1276	2	A39401	metazoa surface
467	65	7.2	1276	2	A39401	metazoa surface

541	63	6.9	767	1	CCORCD	cdcl0_start contc	614	62	6.8	118	2	B69382	hypothetical prote
542	63	6.9	799	2	T02656	probable salt-indu	615	62	6.8	179	2	B83727	hypothetical prote
543	63	6.9	829	2	T01362	probable myosin he	616	62	6.8	201	2	A41656	clindamycin resist
544	63	6.9	832	2	T38749	kinesin-like prote	617	62	6.8	213	2	G64203	chymidine kinase (
545	63	6.9	923	2	T08033	serine/threonine p	618	62	6.8	213	2	F82968	hypothetical prote
546	63	6.9	925	2	T29311	hypothetical prote	619	62	6.8	240	2	T09700	MMS-box protein -
547	63	6.9	979	2	T40006	hypothetical prote	620	62	6.8	246	2	B71084	hypothetical prote
548	63	6.9	987	1	T08830	transposase - Bact	621	62	6.8	268	2	C90516	esterase/lipase 1
549	63	6.9	1028	2	A96719	hypothetical prote	622	62	6.8	293	2	AC1459	conserved hypotet
550	63	6.9	1076	2	A69409	cardamoyl-phosphat	623	62	6.8	316	2	G97050	DNA-methyltransfer
551	63	6.9	1093	1	S50614	regulatory protein	624	62	6.8	326	2	S42531	hem B protein - Sy
552	63	6.9	1095	2	T41171	importin beta subu	625	62	6.8	344	2	E95123	conserved hypotet
553	63	6.9	1095	2	AC03059	hypothetical prote	626	62	6.8	344	2	G97993	hypothetical prote
554	63	6.9	1225	2	A49464	chromosome segrega	627	62	6.8	358	2	S73776	MG269 homolog F11_
555	63	6.9	1284	2	G86145	P22L4.6 protein -	628	62	6.8	365	2	T08679	procollagen-lysine
556	63	6.9	1405	2	T40607	probable dna-dirc	629	62	6.8	384	1	T46966	diene cyclochrome
557	63	6.9	1478	2	T38712	ABC transporter SP	630	62	6.8	390	2	A72108	hypothetical prote
558	63	6.9	1620	2	S21045	complement protein	631	62	6.8	390	2	B86514	hypothetical prote
559	63	6.9	1683	2	AP2071	WD-40 repeat prote	632	62	6.8	402	2	T12745	hypothetical prote
560	63	6.9	1770	2	S45842	Tyb protein - yeas	633	62	6.8	408	2	S33683	site-specific DNA-
561	63	6.9	1927	2	A59236	embryonic muscle m	634	62	6.8	411	2	S07472	alpha-galactosidas
562	63	6.9	2363	2	T38841	probable pre-mRNA	635	62	6.8	413	2	I56481	alpha 1-proteinase
563	63	6.9	4128	2	JCG306	protein kinase (EC	636	62	6.8	415	2	T00140	capsid protein - S
564	63	6.9	6359	2	T31679	bactitracin synthet	637	62	6.8	422	2	AB1154	D-ragatose-bisphos
565	63	6.9	9376	2	T14593	xyringomycin synth	638	62	6.8	427	2	JC4623	prolyl aminopeptid
566	63	6.9	191	2	I37904	c-myc promoter-bin	639	62	6.8	429	2	T04667	cyclin 2b - Arabid
567	63	6.9	206	1	R3EC4	ribosomal protein	640	62	6.8	442	2	T39284	nuclear domain 10
568	63	6.9	206	2	A11008	30S ribosomal chai	641	62	6.8	446	2	A56733	hypothetical prote
569	63	6.9	206	2	A91149	30S ribosomal subu	642	62	6.8	451	2	S43425	tubulin alpha chai
570	63	6.9	206	2	B85994	30S ribosomal subu	643	62	6.8	465	2	S74905	hypothetical prote
571	63	6.9	260	1	S28373	hypothetical prote	644	62	6.8	474	2	A71911	glu-tRNA amidotran
572	63	6.9	260	2	T05559	hypothetical prote	645	62	6.8	495	2	T14894	glucose-6-phosphat
573	63	6.9	285	2	A95851	probable oxidoredu	646	62	6.8	503	1	O4HU19	aromatase (EC 1.14
574	63	6.9	301	2	AE1659	probable Arac-type	647	62	6.8	542	2	AC1704	class I heat-shock
575	63	6.9	302	2	A06898	phosphoglucconate d	648	62	6.8	545	2	T52068	RAN GTPase-activat
576	63	6.9	315	2	G91106	glutathione synthe	649	62	6.8	564	1	KRHUB8	keratin 6b, type I
577	63	6.9	315	2	B85952	glutathione synthe	650	62	6.8	572	2	AC1880	hypothetical prote
578	63	6.9	316	1	STECG5	glutathione syntha	651	62	6.8	577	2	T12536	hypothetical prote
579	63	6.9	346	2	T45069	8-Hydroxy-guanine	652	62	6.8	612	2	B84936	RNA polymerase sig
580	63	6.9	372	2	G90983	GDP-D-mannose dehy	653	62	6.8	617	1	RNUJV7A	transcription init
581	63	6.9	372	2	B85829	GDP-mannose dehydr	654	62	6.8	635	2	T49694	hypothetical prote
582	63	6.9	376	2	T16116	hypothetical prote	655	62	6.8	660	2	A80893	RNA polymerase sig
583	63	6.9	399	2	T38388	hypothetical wd-40	656	62	6.8	668	2	B86777	hypothetical prote
584	63	6.9	400	1	KRHU9	keratin 19, type I	657	62	6.8	712	2	T02312	probable anion exc
585	63	6.9	419	2	T51795	HOMEBOX PROTEIN X	658	62	6.8	728	2	T36026	hypothetical prote
586	63	6.9	445	2	A83078	two-component reep	659	62	6.8	782	2	A34219	ABC excision nucle
587	63	6.9	455	2	T23712	hypothetical prote	660	62	6.8	793	2	S54772	Bic-D protein - fac
588	63	6.9	455	2	G83843	rhomblokinase BHI	661	62	6.8	833	2	S48558	mammary gland fat
589	63	6.9	475	2	F71364	probable RNA polym	662	62	6.8	863	2	AH2296	hypothetical prote
590	63	6.9	480	2	AH1537	Glutamine ABC tran	663	62	6.8	904	2	G64840	protein-histidine
591	63	6.9	483	2	S41853	centromere/microtu	664	62	6.8	904	2	D90772	sensor protein for
592	63	6.9	485	2	T32538	hypothetical prote	665	62	6.8	904	2	H85634	serine/threonine p
593	63	6.9	509	2	S66516	oryzaasin (EC 3.4.2	666	62	6.8	927	2	T08034	regulatory protein
594	63	6.9	578	2	D64993	yfaa protein - Bac	667	62	6.8	980	2	S54986	G-utrophin - mouse
595	63	6.9	583	2	A70380	arginine-tRNA liga	668	62	6.8	987	2	T48373	hypothetical prote
596	63	6.9	591	2	T13650	zinc finger protei	669	62	6.8	1026	2	S51432	transcription regu
597	63	6.9	600	2	T01062	hypothetical prote	670	62	6.8	1121	2	C82120	hypothetical prote
598	63	6.9	627	2	T32958	non-phototropic hy	671	62	6.8	1193	2	T32016	hypothetical prote
599	63	6.9	661	2	T51779	non-phototropic hy	672	62	6.8	1218	2	B84537	hypothetical prote
600	63	6.9	744	2	T12705	NADH2 dehydrogenas	673	62	6.8	1417	2	F96613	hypothetical prote
601	63	6.9	768	2	T02572	hypothetical prote	674	62	6.8	1418	2	T37264	phospholipase C (E
602	63	6.9	841	2	T50358	hypothetical betin	675	62	6.8	1452	2	A97323	DNA polymerase III
603	63	6.9	920	2	F71823	isooleucine-tRNA Ii	676	62	6.8	1509	2	A47224	myosin heavy chain
604	63	6.9	946	1	A47299	tor-related recept	677	62	6.8	1768	2	T50074	probable nucleopor
605	63	6.9	970	2	A36417	Na+/Ca2+-exchangin	678	62	6.8	1790	1	S27772	vitelllogenin precu
606	63	6.9	970	2	S27114	Na+/Ca2+-exchangin	679	62	6.8	1864	2	F86378	protein F219.12 [
607	63	6.9	970	2	I48097	Na+/Ca2+-exchangin	680	62	6.8	1957	2	T38077	hypothetical colle
608	63	6.9	1064	2	H64516	hypothetical prote	681	62	6.8	2823	2	F87908	protein T22A3.8 [i
609	63	6.9	1068	2	F84614	probable kinesin h	682	62	6.8	2823	2	T33064	hypothetical prote
610	63	6.9	1503	2	T43166	alpha-2-macroglobu	683	62	6.8	2954	2	T14156	kinesin-related pr
611	63	6.9	1959	1	A31977	myosin heavy chain	684	62	6.8	3102	2	T43291	laminin alpha chai
612	63	6.9	1976	2	A59252	myosin heavy chain	685	62	6.8	3433	1	S28381	utrophin - human
613	63	6.9	4464	2	D87755	protein T21E12.4 [686	61.5	6.8	155	2	B83771	hypothetical prote

687	61.5	6.8	163	2	S39821	tubulin beta chain	760	61	6.7	435	2	H87516	D-alanyl-D-alanine
688	61.5	6.8	169	2	B91104	probable transcript	761	61	6.7	438	2	A12049	substrate-binding
689	61.5	6.8	169	2	H85949	probable transcript	762	61	6.7	452	2	S47236	ribulose-bisphosph
690	61.5	6.8	242	2	AC2464	hypothetical prote	763	61	6.7	461	2	D72414	anthranilate synth
691	61.5	6.8	269	2	A84841	probable embryo-ab	764	61	6.7	489	1	QJ1289	riamulokinase (EC
692	61.5	6.8	273	2	T48693	mitochondrial inhe	765	61	6.7	509	2	T12521	hypothetical prote
693	61.5	6.8	306	2	T49541	hypothetical prote	766	61	6.7	517	2	T07704	hypothetical prote
694	61.5	6.8	325	2	T15296	hypothetical prote	767	61	6.7	522	2	JS0450	replication initia
695	61.5	6.8	347	2	B72596	hypothetical prote	768	61	6.7	528	2	S73270	chaperonin, 60K -
696	61.5	6.8	352	2	US0637	RepB protein - Thi	769	61	6.7	530	2	T50435	conserved hypotnet
697	61.5	6.8	355	2	A41534	GTP-binding protei	770	61	6.7	549	2	A70358	topoisomerase I -
698	61.5	6.8	406	2	T21271	hypothetical prote	771	61	6.7	562	2	AH2084	hypothetical prote
699	61.5	6.8	425	1	KRX12A	keratin, 64K type	772	61	6.7	591	2	D89783	RBD-containing lip
700	61.5	6.8	426	2	E70058	ubiquitin-cytochro	773	61	6.7	599	2	G83550	GTP-binding protei
701	61.5	6.8	445	2	A41896	transcription acti	774	61	6.7	612	2	AP0079	RNA polymerase sig
702	61.5	6.8	467	2	A49901	NBR1 mobilization	775	61	6.7	615	1	RNEB8T	transcription init
703	61.5	6.8	495	2	AD3038	alpha-amyase amya	776	61	6.7	644	2	B31794	mfm-1 protein (C10
704	61.5	6.8	506	2	G98247	cytoplasmic alpha-	777	61	6.7	676	2	JC7222	77K muscle-derived
705	61.5	6.8	508	2	T40249	hypothetical prote	778	61	6.7	689	2	A31794	mfm-1 nuclear prot
706	61.5	6.8	525	2	G95374	probable ABC trans	779	61	6.7	691	2	B6152	T7123.14 protein -
707	61.5	6.8	537	2	B84772	probable DnaJ prot	780	61	6.7	695	2	JC1493	foliitropin recept
708	61.5	6.8	539	2	S58287	U-domain protein D	781	61	6.7	695	2	G87316	nuclease, probable
709	61.5	6.8	551	2	S67788	hypothetical prote	782	61	6.7	708	2	S53411	hypothetical prote
710	61.5	6.8	566	2	T23926	hemagglutinin-neur	783	61	6.7	794	2	G02317	transcription acti
711	61.5	6.8	571	1	HNNZP2	hemagglutinin-neur	784	61	6.7	805	2	S48411	SBC6 protein - yea
712	61.5	6.8	571	1	HNNZT2	probable two-compo	785	61	6.7	820	2	I48347	protein-lysine K
713	61.5	6.8	588	2	D82958	conserved hypotnet	786	61	6.7	824	2	C86529	glycogen phosphory
714	61.5	6.8	601	2	B81723	conserved hypotnet	787	61	6.7	824	2	C72095	phosphorylase (EC
715	61.5	6.8	707	2	T21217	hypothetical prote	788	61	6.7	839	2	T39190	probable ATP-depen
716	61.5	6.8	744	2	T13570	MDH2 dehydrogenas	789	61	6.7	856	1	F64098	endopeptidase Clp
717	61.5	6.8	806	1	A64078	endopeptidase La (790	61	6.7	860	2	S76534	hypothetical prote
718	61.5	6.8	846	2	JC7720	DNA topoisomerase	791	61	6.7	882	2	I38912	receptor tyrosine
719	61.5	6.8	858	2	B72419	acetyltransferase	792	61	6.7	886	2	C84517	probable receptor-
720	61.5	6.8	877	2	T01271	serine/threonine-s	793	61	6.7	905	2	T23510	hypothetical prote
721	61.5	6.8	877	2	T01271	sugar hydroxylase ho	794	61	6.7	933	2	S49461	synaptonemal compl
722	61.5	6.8	882	2	PC1231	hexokinase (EC 2.7	795	61	6.7	999	2	I38547	novel cellular pro
723	61.5	6.8	924	1	S13913	hypothetical prote	796	61	6.7	1042	2	A49204	translational elonga
724	61.5	6.8	972	2	C71826	Na+/Ca2+-exchangin	797	61	6.7	1179	2	G95144	conserved hypotnet
725	61.5	6.8	973	2	S32815	beta-galactosidase	798	61	6.7	1213	2	S42368	guanine nucleotide
726	61.5	6.8	1034	2	T10551	beta-galactosidase	799	61	6.7	1388	2	T30335	KLP2 protein - Afr
727	61.5	6.8	1034	2	A24925	probable ATPase F2	800	61	6.7	1564	2	S55517	probable transport
728	61.5	6.8	1123	2	C96622	ATP-dependent deox	801	61	6.7	1648	2	F84833	probable SNF2/SW12
729	61.5	6.8	1235	2	AC1728	insulin receptor-r	802	61	6.7	1666	2	T43169	hypothetical prote
730	61.5	6.8	1268	2	B36502	RNA-directed RNA p	803	61	6.7	1787	2	AC2009	serine/threonine k
731	61.5	6.8	1323	1	BRWGSM	DNA-directed RNA p	804	61	6.7	2109	2	B89066	protein H05009.1 [
732	61.5	6.8	1388	2	G70633	hypothetical prote	805	61	6.7	2189	2	T33247	hypothetical prote
733	61.5	6.8	1391	2	C82007	myosin heavy chain	806	61	6.7	2388	2	JB0271	beta spectrin, bet
734	61.5	6.8	1445	2	T15212	nonstructural poly	807	61	6.7	3187	2	JC5837	364K Golgi complex
735	61.5	6.8	1495	1	MMW62	cytoplasmic dynein	808	61	6.7	149	2	E98191	hypothetical prote
736	61.5	6.8	1979	1	MMW62	hypothetical prote	809	61	6.7	149	2	E98191	conserved hypotnet
737	61.5	6.8	2514	1	MMW62	uridine-monophosph	810	61	6.7	178	2	F97325	amidease from nicot
738	61.5	6.8	4540	2	T30838	hypothetical prote	811	61	6.7	185	2	A83267	probable transcript
739	61.5	6.8	183	2	H97046	hypothetical prote	812	61	6.7	206	2	B97282	ribosomal protein
740	61.5	6.7	201	2	B86488	hypothetical prote	813	61	6.7	206	2	G81229	30S ribosomal prot
741	61.5	6.7	204	2	A33572	oxidoreductase	814	61	6.7	219	2	JQ1075	S2 protein - garde
742	61.5	6.7	210	2	B64639	hypothetical prote	815	61	6.7	248	2	F71026	hypothetical prote
743	61.5	6.7	219	2	F69341	conserved hypotnet	816	61	6.7	258	2	I46080	uroplakin Ia - bov
744	61.5	6.7	244	1	T01091	MDH2 dehydrogenas	817	61	6.7	270	2	A34717	meiotic recombinat
745	61.5	6.7	250	2	G83283	precortin-2 methyl	818	61	6.7	279	2	T14332	homeotic protein -
746	61.5	6.7	253	1	G70106	coar protein - cas	819	61	6.7	292	2	T52257	CCR4-associated fa
747	61.5	6.7	258	2	VCOMCN	MDH2 dehydrogenas	820	61	6.7	305	2	B72365	clostridia-relate
748	61.5	6.7	260	2	T12427	hypothetical prote	821	61	6.7	322	2	E69496	porphobilinogen sy
749	61.5	6.7	287	2	S74050	hypothetical prote	822	61	6.7	375	1	C69512	musonate cyclisom
750	61.5	6.7	326	2	AC1819	hypothetical prote	823	61	6.7	376	2	T47519	hypothetical prote
751	61.5	6.7	345	2	T46962	8-oxoguanine DNA-g	824	61	6.7	385	2	A71107	hypothetical prote
752	61.5	6.7	357	2	A84551	hypothetical prote	825	61	6.7	386	2	G88765	protein T1187.1 [i
753	61.5	6.7	368	2	H83781	conserved hypotnet	826	61	6.7	388	2	T22795	glucocorticoid-act
754	61.5	6.7	370	2	H82291	keratin 6d, type I	827	61	6.7	403	2	S71356	tRNA nucleotidyl t
755	61.5	6.7	384	2	161769	2',3'-cyclic-nucle	828	61	6.7	412	2	C91121	genome polypotein
756	61.5	6.7	400	1	ESBOP3	transposase, ISC131	829	61	6.7	426	2	B85966	ATP-dependent nucl
757	61.5	6.7	411	2	C90458	hypothetical prote	830	61	6.7	430	2	C64554	hypothetical prote
758	61.5	6.7	416	2	T20300	hypothetical prote	831	61	6.7	431	2	C71954	hypothetical prote
759	61.5	6.7	435	2	H75006	methyl-accepting c	832	61	6.7	431	2	C71954	hypothetical prote

833	60.5	6.7	437	2	T08094	probable sulfate a	906	60	6.6	336	2	S41643	85M protein - Rhi
834	60.5	6.7	445	2	B71642	hypothetical prote	907	60	6.6	335	2	G71804	translational elonga
835	60.5	6.7	445	2	T24829	hypothetical prote	908	60	6.6	335	2	G71828	probable tRNA (5-m
836	60.5	6.7	449	2	T16891	protein phosphatas	909	60	6.6	360	2	G64686	conserved hypotet
837	60.5	6.7	486	2	H85719	probable oxidoredu	910	60	6.6	360	2	F70045	two-component sens
838	60.5	6.7	486	2	G90897	probable oxidoredu	911	60	6.6	374	2	B89971	conserved hypotet
839	60.5	6.7	496	2	AC1968	carboxy-terminal p	912	60	6.6	384	2	C82385	mannitol-1-phospha
840	60.5	6.7	512	2	C41968	transcription acti	913	60	6.6	394	2	G71528	probable translati
841	60.5	6.7	520	1	G86662	2',3'-cyclic-nucle	914	60	6.6	409	2	T28355	ORF MSV194 Ali mot
842	60.5	6.7	520	2	AG1249	hypothetical prote	915	60	6.6	452	2	S47224	ribose-bisphosph
843	60.5	6.7	520	2	AC1612	hypothetical prote	916	60	6.6	452	2	S47233	glucanate dehydrat
844	60.5	6.7	524	2	A45472	protein kinase (EC	917	60	6.6	455	1	A69753	alpha-galactosidas
845	60.5	6.7	530	2	T42208	propionyl-CoA carb	918	60	6.6	471	2	J01021	hypothetical prote
846	60.5	6.7	544	2	A41905	hypothetical prote	919	60	6.6	475	2	T32036	hypothetical prote
847	60.5	6.7	545	2	E97728	DNA repair protein	920	60	6.6	491	2	A40594	probable molybdenu
848	60.5	6.7	578	2	S44975	lmcC protein - Str	921	60	6.6	502	2	S49113	hypothetical prote
849	60.5	6.7	611	2	B85077	probable reverse t	922	60	6.6	515	2	T52610	glucose-6-phosphat
850	60.5	6.7	616	2	D85897	hypothetical prote	923	60	6.6	521	2	T04791	hypothetical prote
851	60.5	6.7	616	2	H91052	molecular chaperon	924	60	6.6	531	2	C70333	hypothetical prote
852	60.5	6.7	616	2	B65029	heat shock cognate	925	60	6.6	589	2	T48905	gamma response 1 p
853	60.5	6.7	624	2	T00044	vacuolar sorting r	926	60	6.6	621	2	S35092	plakoglobin - mous
854	60.5	6.7	628	2	D86466	69.4K hypothetical	927	60	6.6	625	2	T21051	hypothetical prote
855	60.5	6.7	646	2	B82168	two-component hybr	928	60	6.6	645	2	G88130	protein F10G7.4 (i
856	60.5	6.7	650	2	A00352	chaperone protein	929	60	6.6	682	2	F90603	virulence-like (mycopla
857	60.5	6.7	655	2	P83597	hypothetical prote	930	60	6.6	685	2	A71901	probable flagellar
858	60.5	6.7	687	2	S43250	thimet oligopeptid	931	60	6.6	710	2	A41109	anaerobic ribonucel
859	60.5	6.7	726	2	A97041	exodeoxyribonuclea	932	60	6.6	715	2	T31819	hypothetical prote
860	60.5	6.7	737	2	B61678	heavy metal-transp	933	60	6.6	725	2	A47168	cardiac morphogene
861	60.5	6.7	816	2	S54518	probable membrane	934	60	6.6	741	2	T13251	NADH2 dehydrogenas
862	60.5	6.7	835	1	I57441	involutrin - orang	935	60	6.6	745	2	I57655	Sertoli cell leuci
863	60.5	6.7	881	2	T03461	methyl-accepting c	936	60	6.6	757	1	S41712	myb-related protei
864	60.5	6.7	907	1	VGBBTE	glycoprotein B pre	937	60	6.6	881	2	T31739	hypothetical prote
865	60.5	6.7	924	2	C86725	chromosome segrega	938	60	6.6	960	1	S28262	kinesin-related pr
866	60.5	6.7	926	2	D86897	hypothetical prote	939	60	6.6	963	2	T41479	RAD6 nucleotide e
867	60.5	6.7	930	2	T32017	hypothetical prote	940	60	6.6	996	2	AG2366	hypothetical prote
868	60.5	6.7	938	1	SYECIT	isoleucine-tRNA li	941	60	6.6	1036	2	D70117	acridiflavine resist
869	60.5	6.7	967	2	D96573	protein p12M16.21	942	60	6.6	1088	1	P1XRSR	inner layer protei
870	60.5	6.7	1083	2	UC2300	cell surface glyco	943	60	6.6	1178	2	S30431	MSP-300 protein -
871	60.5	6.7	1116	2	D97001	probable membrane	944	60	6.6	1192	2	T48499	receptor-like prot
872	60.5	6.7	1117	2	T14891	telomerase (EC 2.7	945	60	6.6	1237	2	H81660	DNA polymerase III
873	60.5	6.7	1138	2	D85584	probable tail comp	946	60	6.6	1251	2	A56677	neuronal cell cycl
874	60.5	6.7	1162	2	D83454	conserved hypotet	947	60	6.6	1268	2	T31420	C-terminal domain-
875	60.5	6.7	1164	2	T06144	disease resistance	948	60	6.6	1436	2	S57655	probable membrane
876	60.5	6.7	1177	2	A00438	probable exported	949	60	6.6	1437	2	F69680	DNA-directed DNA p
877	60.5	6.7	1186	2	T23327	adenomatous polyo	950	60	6.6	1582	2	AC1153	adhesin homolog 1m
878	60.5	6.7	1235	2	AC1358	ATP-dependent deox	951	60	6.6	1707	2	S77908	hypothetical prote
879	60.5	6.7	1270	2	T26720	hypothetical prote	952	60	6.6	1753	2	T00350	hypothetical prote
880	60.5	6.7	1355	2	S51995	probable ATPase (E	953	60	6.6	1759	2	T18868	myoblast cily prot
881	60.5	6.7	1388	2	S74245	serine/threonine-s	954	60	6.6	1876	2	T28627	vitellogenin - Rfp
882	60.5	6.7	1391	2	F81233	DNA-directed RNA p	955	60	6.6	2186	2	T31659	clggrin - fruit fl
883	60.5	6.7	1440	2	UC6312	protein-tyrosine-p	956	60	6.6	2434	2	T42759	Munc13-3 protein -
884	60.5	6.7	1498	2	S78102	chitin synthase (E	957	60	6.6	2207	2	S44861	DNA topoisomerase
885	60.5	6.7	1650	2	S28721	hypothetical prote	958	60	6.6	3329	2	T42205	breast cancer susc
886	60.5	6.7	1759	2	T03725	replisase polyprot	959	60	6.6	3587	2	T31075	tyrosidine synthet
887	60.5	6.7	2151	1	S16449	genome polyprotein	960	60	6.6	76	2	P90062	conserved hypotet
888	60.5	6.7	2297	2	A82494	hypothetical prote	961	60	6.6	123	2	D86407	hypothetical prote
889	60.5	6.7	3078	2	T28432	variant-specific s	962	60	6.6	175	2	AD1800	transcription regu
890	60.5	6.7	3335	2	H81702	adherence factor T	963	60	6.6	201	2	G87641	transcription regu
891	60.5	6.7	3519	2	S43048	polyketide synthas	964	60	6.6	228	2	D87488	ABC transporter. A
892	60.5	6.7	3519	2	D36950	ureB protein - Bac	965	60	6.6	241	2	B69484	hypothetical prote
893	60.5	6.6	148	2	A71876	probable aldehyde	966	60	6.6	245	2	G64471	cell division prot
894	60.5	6.6	216	2	U01076	S3 protein - garde	967	60	6.6	262	1	A13172	granzyme A (EC 3.4
895	60.5	6.6	219	2	D88990	protein C36C5.12 l	968	60	6.6	279	2	G66406	unknown protein (i
896	60.5	6.6	224	2	B84363	H+-transporting AT	969	60	6.6	288	2	C66687	hypothetical prote
897	60.5	6.6	234	2	C75552	hypothetical prote	970	60	6.6	291	2	S75791	hypothetical prote
898	60.5	6.6	234	2	A84515	probable MADS-box	971	60	6.6	293	2	G70444	hypothetical prote
899	60.5	6.6	260	2	T12443	NADH2 dehydrogenas	972	60	6.6	324	2	A80554	probable oxidoredu
900	60.5	6.6	260	2	T12431	NADH2 dehydrogenas	973	60	6.6	335	2	C64380	porphobilinogen by
901	60.5	6.6	260	2	T12429	NADH2 dehydrogenas	974	60	6.6	368	2	T20182	hypothetical prote
902	60.5	6.6	261	2	AF1939	hypothetical prote	975	60	6.6	369	1	ESBYPc	3',5'-cyclic-nucle
903	60.5	6.6	262	2	E70365	geranylgeranyl pyr	976	60	6.6	378	2	A44443	basic helix-loop-h
904	60.5	6.6	276	2	D70618	hypothetical prote	977	60	6.6	397	2	S66700	probable membrane
905	60.5	6.6	277	2	S75803	hypothetical prote	978	60	6.6	400	2	B88769	protein C53B4.7 (i

979	59.5	6.6	404	2	A64151	hypothetical prote	1052	59.5	6.6	1951	2	B43963	RNA viral polymera
980	59.5	6.6	412	1	KRSHL1	keratin_48k type	1053	59.5	6.6	2116	2	A26555	myosin heavy chain
981	59.5	6.6	419	2	D45045	phycobiliprotein h	1054	59.5	6.6	2150	2	S13553	hypothetical prote
982	59.5	6.6	437	1	S73806	cysteine-cRNA liga	1055	59.5	6.6	2253	2	T30336	nuclear/mitotic ap
983	59.5	6.6	437	2	UC1165	alte-specific DNA-	1056	59.5	6.6	2512	1	MNWS	nonstructural poly
984	59.5	6.6	438	2	T47861	nucleolar autoanti	1057	59.5	6.6	2663	1	S28261	centromere protein
985	59.5	6.6	441	2	T32021	hypothetical prote	1058	59.5	6.6	2632	2	B49132	fat facets (faf) s
986	59.5	6.6	459	2	A89863	argininosuccinate	1059	59.5	6.6	2829	2	A42771	reticulocyte-bind
987	59.5	6.6	459	2	T31608	hypothetical prote	1060	59.5	6.6	4687	1	A39638	plectin - rat
988	59.5	6.6	464	2	H83752	glutamate dehydrog	1061	59	6.5	144	2	T14170	1-aminocyclopropan
989	59.5	6.6	475	1	B64602	petit1-like protei	1062	59	6.5	199	2	D70466	ribosomal protein
990	59.5	6.6	493	2	S74652	hypothetical prote	1063	59	6.5	203	2	S43222	hypothetical prote
991	59.5	6.6	498	2	AH0952	conserved hypotne	1064	59	6.5	209	2	S75029	hypothetical prote
992	59.5	6.6	512	2	C91268	transcription acti	1065	59	6.5	216	1	KIBYR8	dTMP kinase (EC 2.
993	59.5	6.6	512	2	A86109	transcription acti	1066	59	6.5	224	2	T17983	hypothetical protei
994	59.5	6.6	530	2	T32031	hypothetical prote	1067	59	6.5	227	2	C29224	GTP-binding protei
995	59.5	6.6	540	2	T50617	hypothetical prote	1068	59	6.5	244	2	B85926	3'-phosphadenosin
996	59.5	6.6	540	2	B97994	DNA primase (EC 2.	1069	59	6.5	244	2	A91081	3'-phosphadenosin
997	59.5	6.6	592	2	H84018	Mg-protoporphyrin	1070	59	6.5	247	1	QQCVR1	coat protein - tom
998	59.5	6.6	595	2	T52327	pectinesterase (EC	1071	59	6.5	251	1	QQCVR2	coat protein - pot
999	59.5	6.6	595	2	T02183	probable pectinest	1072	59	6.5	251	1	QQCVR2	coat protein - equ
1000	59.5	6.6	621	2	S71215	cellulase (EC 3.2.	1073	59	6.5	254	2	T12688	hypothetical prote
1001	59.5	6.6	623	2	C98048	hypothetical prote	1074	59	6.5	260	2	T12428	hypothetical prote
1002	59.5	6.6	649	2	D96914	chemotaxis protein	1075	59	6.5	260	2	T12424	MDH2 dehydrogenas
1003	59.5	6.6	659	2	T16626	hypothetical prote	1076	59	6.5	260	2	F85630	hypothetical prote
1004	59.5	6.6	690	2	S28222	beta-adrenergic-re	1077	59	6.5	301	2	A97412	hypothetical prote
1005	59.5	6.6	700	1	A41615	peroxidase (EC 1.1	1078	59	6.5	315	2	D71525	probable integrase
1006	59.5	6.6	701	2	S62460	hypothetical prote	1079	59	6.5	322	2	S72271	proteoglycan lb pr
1007	59.5	6.6	718	2	A81122	hypothetical prote	1080	59	6.5	325	2	T36495	hypothetical prote
1008	59.5	6.6	739	2	A26016	lysine decarboxyla	1081	59	6.5	329	2	A11892	hypothetical prote
1009	59.5	6.6	742	2	T13245	MDH2 dehydrogenas	1082	59	6.5	341	2	T41450	hypothetical prote
1010	59.5	6.6	744	2	T12611	MDH2 dehydrogenas	1083	59	6.5	346	2	T37430	hydroxysteroid deh
1011	59.5	6.6	744	2	T13376	MDH2 dehydrogenas	1084	59	6.5	356	1	A42053	gap junction prote
1012	59.5	6.6	754	2	S63231	hypothetical prote	1085	59	6.5	360	2	T17996	hypothetical prote
1013	59.5	6.6	776	2	C69072	anaerobic ribonuci	1086	59	6.5	393	2	T38663	probable transacti
1014	59.5	6.6	779	2	AG1978	hypothetical prote	1087	59	6.5	394	2	UC1420	translation elonga
1015	59.5	6.6	838	2	JC7363	95K retinoblastoma	1088	59	6.5	399	2	C90455	transposase ISCl31
1016	59.5	6.6	849	2	G64342	hypothetical prote	1089	59	6.5	403	2	B90290	transposase ISCl31
1017	59.5	6.6	875	2	A53901	ribonuclease P (EC	1090	59	6.5	405	2	AD2164	hypothetical prote
1018	59.5	6.6	891	2	JC6519	DNA topoisomerase	1091	59	6.5	411	2	C90252	conserved hypotnet
1019	59.5	6.6	899	2	A44879	retinoblastoma pro	1092	59	6.5	413	2	AC2360	hypothetical prote
1020	59.5	6.6	938	2	D85483	isoleucine RNA sy	1093	59	6.5	419	2	F72089	hypothetical prote
1021	59.5	6.6	938	2	E90632	isooleucine RNA sy	1094	59	6.5	419	2	F86534	hypothetical prote
1022	59.5	6.6	955	2	S44622	C50C3.3 protein -	1095	59	6.5	423	1	UBFYA	tubulin alpha-1 ch
1023	59.5	6.6	985	2	A96777	hypothetical prote	1096	59	6.5	449	2	S02130	tubulin alpha chai
1024	59.5	6.6	986	2	A82209	two-component sens	1097	59	6.5	449	2	S04474	tubulin alpha-2 ch
1025	59.5	6.6	991	2	T40229	arginyl endopeptid	1098	59	6.5	458	2	C69123	conserved hypotnet
1026	59.5	6.6	1024	2	T43517	kinasin-related pr	1099	59	6.5	458	2	S57605	probable membrane
1027	59.5	6.6	1025	2	B54718	dihydropyrimidine	1100	59	6.5	461	2	B72625	conserved hypotnet
1028	59.5	6.6	1073	1	OYRHUX	heat-stable entero	1101	59	6.5	470	2	S72279	conserved hypotnet
1029	59.5	6.6	1081	2	S66736	transcription acti	1102	59	6.5	472	2	F82807	homolysin secretio
1030	59.5	6.6	1119	2	T14321	nuclear matrix con	1103	59	6.5	473	1	F82561	ribulose-bisphosph
1031	59.5	6.6	1127	2	T28317	ORF MSV156 hypotne	1104	59	6.5	475	1	RKXHLK	ribulose-bisphosph
1032	59.5	6.6	1173	1	A53430	1-phosphatidylinos	1105	59	6.5	475	1	RKSLZL	ribulose-bisphosph
1033	59.5	6.6	1198	2	T43484	hypothetical prote	1106	59	6.5	475	1	RKSLZL	two-component sens
1034	59.5	6.6	1225	2	A56514	chromokinesin - ch	1107	59	6.5	479	2	AD1263	hypothetical prote
1035	59.5	6.6	1233	2	T30534	chromosome segrega	1108	59	6.5	492	2	T32523	probable alanine a
1036	59.5	6.6	1259	2	H65233	ytFN protein - Bgc	1109	59	6.5	505	2	T37975	probable alanine a
1037	59.5	6.6	1259	2	G86119	hypothetical prote	1110	59	6.5	508	1	A36121	aromatase (EC 1.14
1038	59.5	6.6	1259	2	G91278	hypothetical prote	1111	59	6.5	513	2	S08381	keratin_58k type
1039	59.5	6.6	1276	2	T18526	SREBP cleavage act	1112	59	6.5	534	2	I37942	keratin 4, type II
1040	59.5	6.6	1379	2	S64603	YTA7 protein - Yea	1113	59	6.5	534	2	S60205	phosphonacetaldel
1041	59.5	6.6	1401	2	T30247	Werner syndrome pr	1114	59	6.5	554	2	B82934	hypothetical prote
1042	59.5	6.6	1415	2	C86438	hypothetical prote	1115	59	6.5	571	1	D86164	hypothetical prote
1043	59.5	6.6	1481	2	H83017	glutamate synthase	1116	59	6.5	591	1	SYBYKT	lysine-cRNA ligase
1044	59.5	6.6	1514	2	S70099	hypothetical prote	1117	59	6.5	592	2	G35115	hypothetical prote
1045	59.5	6.6	1526	2	S49763	gatingpain R (EC 3.	1118	59	6.5	620	1	F86269	hypothetical prote
1046	59.5	6.6	1679	2	S49802	probable membrane	1119	59	6.5	621	1	S73825	hypothetical prote
1047	59.5	6.6	1704	2	A55426	gatingpain R (EC 3.	1120	59	6.5	623	2	S67762	hypothetical prote
1048	59.5	6.6	1742	2	T49451	kinasin-like prote	1121	59	6.5	639	2	B86587	DNA helicase (lmo
1049	59.5	6.6	1893	1	A40262	transcription init	1122	59	6.5	639	2	G72038	ATP-dependent heli
1050	59.5	6.6	1906	1	S68235	myosin-light-chain	1123	59	6.5	642	2	T41690	conserved hypotnet
1051	59.5	6.6	1908	2	A86311	protein FIL3.14 [1	1124	59	6.5	647	2	C83012	probable chemotaxi

1125	59	6.5	654	2	B56011	transcription fact	1198	58.5	6.4	404	2	T19480	hypothetical prote
1126	59	6.5	672	2	C72404	glycine-tRNA ligas	1199	58.5	6.4	409	2	B59433	conserved hypotet
1127	59	6.5	692	2	T41240	hypothetical zinc	1200	58.5	6.4	413	2	T26072	hypothetical prote
1128	59	6.5	695	2	T45896	follicle stimulat	1201	58.5	6.4	415	1	O4PSCP	campfor 5-monooxy
1129	59	6.5	741	2	T12762	NADH2 dehydrogen	1202	58.5	6.4	431	2	T26071	hypothetical prote
1130	59	6.5	743	2	T13700	NADH2 dehydrogen	1203	58.5	6.4	458	2	G83997	exodeoxyribonucle
1131	59	6.5	758	2	F72363	hypothetical prote	1204	58.5	6.4	458	2	S57914	probable sakacin P
1132	59	6.5	759	1	B60008	RNA-directed RNA p	1205	58.5	6.4	458	2	S56816	Grpase-activating
1133	59	6.5	759	1	P31V68	RNA-directed RNA p	1206	58.5	6.4	468	2	UC4285	acid phosphatase (
1134	59	6.5	759	2	G86781	5-methyltetrahydro	1207	58.5	6.4	468	2	S55695	suppressor of fuse
1135	59	6.5	762	2	A96634	probable GCNA-comp	1208	58.5	6.4	474	2	B69470	lipase homolog - A
1136	59	6.5	790	2	E48327	COI intron A proce	1209	58.5	6.4	479	1	IXBE1F	alpha trans-induci
1137	59	6.5	814	2	T00740	hypothetical prote	1210	58.5	6.4	481	2	IXBE1F	hypothetical prote
1138	59	6.5	826	2	T23072	hypothetical prote	1211	58.5	6.4	486	2	A64909	probable fructuron
1139	59	6.5	835	2	S40144	hypothetical prote	1212	58.5	6.4	489	1	S66088	conserved hypotet
1140	59	6.5	860	2	AB2044	ribonucleoside-dip	1213	58.5	6.4	489	2	P97118	levanucrase (limp
1141	59	6.5	868	2	A84518	adenylate cyclase	1214	58.5	6.4	490	1	IXBE17	alpha trans-induci
1142	59	6.5	887	2	B96598	probable receptor	1215	58.5	6.4	490	2	I41293	EcoE type I restri
1143	59	6.5	890	1	A53743	hypothetical prote	1216	58.5	6.4	497	2	C70454	transcription regu
1144	59	6.5	897	2	S02032	protein-tyrosine k	1217	58.5	6.4	500	2	B31047	testosterone 16alp
1145	59	6.5	931	2	H96527	alpha-actinin 2, s	1218	58.5	6.4	505	1	S13744	glucose-6-phosphat
1146	59	6.5	944	2	S26710	protein F27015.16	1219	58.5	6.4	508	2	I53018	steroid 17 alpha-h
1147	59	6.5	971	2	T09210	spindle pole body	1220	58.5	6.4	508	2	S52756	steroid 17alpha-mo
1148	59	6.5	996	2	T47518	serine/threonine p	1221	58.5	6.4	512	2	S70644	annexin VII - Afri
1149	59	6.5	1075	1	OYRTHX	heat-stable entero	1222	58.5	6.4	516	2	T52611	glucose-6-phosphat
1150	59	6.5	1076	2	JC2217	major surface glyco	1223	58.5	6.4	522	2	T18657	hypothetical prote
1151	59	6.5	1117	2	A38227	RNA-splicing regul	1224	58.5	6.4	522	2	D96602	nucleolar protein
1152	59	6.5	1117	1	A43736	creatine kinase (E	1225	58.5	6.4	529	2	G70140	oligopeptidase ABC t
1153	59	6.5	1331	1	XORTDH	xanthine dehydroge	1226	58.5	6.4	530	2	B96616	hypothetical prote
1154	59	6.5	1331	1	XOWSDH	xanthine dehydroge	1227	58.5	6.4	560	2	B64600	soluble lytic mure
1155	59	6.5	1348	2	B23496	TyB protein - yeas	1228	58.5	6.4	569	1	S62851	hypothetical prote
1156	59	6.5	1435	2	S59384	hypothetical prote	1229	58.5	6.4	570	2	A48836	flitropellin C prec
1157	59	6.5	1458	2	A45665	adult-specific Bru	1230	58.5	6.4	578	2	T21345	hypothetical prote
1158	59	6.5	1493	2	S49777	probable membrane	1231	58.5	6.4	581	2	B72221	hypothetical prote
1159	59	6.5	1496	2	T05634	hypothetical prote	1232	58.5	6.4	591	2	T51996	hypothetical prote
1160	59	6.5	1660	2	A84647	hypothetical prote	1233	58.5	6.4	591	2	T41531	activator of Hsp70
1161	59	6.5	1679	2	S48385	hypothetical prote	1234	58.5	6.4	624	1	BHTE	hemocyanin chain e
1162	59	6.5	1735	2	A57607	Munc13-1 - rat	1235	58.5	6.4	688	2	T13708	hypothetical prote
1163	59	6.5	1770	2	S58651	TyB protein - yeas	1236	58.5	6.4	709	2	S03812	hypothetical prote
1164	59	6.5	1770	2	S69966	TyB protein - yeas	1237	58.5	6.4	714	2	AP2458	exonuclease ABC c
1165	59	6.5	1771	2	S53592	TyB protein - yeas	1238	58.5	6.4	717	1	S29923	transforming prote
1166	59	6.5	1780	2	T17272	hypothetical prote	1239	58.5	6.4	717	2	T33295	hypothetical prote
1167	59	6.5	2109	2	T18414	transcription fact	1240	58.5	6.4	746	2	T13678	NADH2 dehydrogen
1168	59	6.5	2364	1	A44159	spectrin beta-g ch	1241	58.5	6.4	758	2	AB0167	ATP-dependent Clp
1169	59	6.5	2413	2	S34670	splicing factor PR	1242	58.5	6.4	778	2	F95168	cation-transportin
1170	59	6.5	2442	2	T08621	centriosome associa	1243	58.5	6.4	780	2	G98054	P-type ATPase, met
1171	59	6.4	136	2	T13419	hypothetical prote	1244	58.5	6.4	810	2	C70791	probable pona', pro
1172	58.5	6.4	150	2	H83774	hypothetical prote	1245	58.5	6.4	844	2	C84685	probable beta-gala
1173	58.5	6.4	180	2	G90185	DNA-directed RNA p	1246	58.5	6.4	844	1	TYMSVY	transforming prote
1174	58.5	6.4	181	2	H87384	acetyltransferase,	1247	58.5	6.4	865	2	A25762	regulatory protein
1175	58.5	6.4	206	2	B83113	30S ribosomal prot	1248	58.5	6.4	871	2	S68482	probable membrane
1176	58.5	6.4	206	2	B82061	ribosomal protein	1249	58.5	6.4	902	1	S54495	probable carrier p
1177	58.5	6.4	210	2	C70528	hypothetical prote	1250	58.5	6.4	902	2	A55543	cmaA protein - Pse
1178	58.5	6.4	237	2	H64363	hypothetical prote	1251	58.5	6.4	913	1	A41109	protein-tyrosine-p
1179	58.5	6.4	241	2	F71558	probable tRNA penu	1252	58.5	6.4	947	2	T20156	hypothetical prote
1180	58.5	6.4	260	2	S60480	low temperature-in	1253	58.5	6.4	963	2	AR2119	hypothetical prote
1181	58.5	6.4	263	2	T47074	hypothetical prote	1254	58.5	6.4	970	1	QZ2M	phosphoenolpyruvat
1182	58.5	6.4	276	2	B83430	cytochrome-c oxida	1255	58.5	6.4	972	2	T39876	hypothetical prote
1183	58.5	6.4	290	1	D47468	cytochrome-c oxida	1256	58.5	6.4	974	1	A49714	protein-tyrosine k
1184	58.5	6.4	290	2	S53904	hypothetical prote	1257	58.5	6.4	993	2	J02169	RNA 1 protein - cu
1185	58.5	6.4	312	2	T00992	hypothetical prote	1258	58.5	6.4	1008	2	F71727	acetylflavin resista
1186	58.5	6.4	315	2	AC2537	chromosome partiti	1259	58.5	6.4	1032	1	G7BP14	baeapilatin protei
1187	58.5	6.4	336	2	H72618	hypothetical prote	1260	58.5	6.4	1034	2	T30574	beta-galactosidase
1188	58.5	6.4	336	2	C64870	probable splicing	1261	58.5	6.4	1035	2	I58409	integrin alpha-9 c
1189	58.5	6.4	365	2	D97848	hypothetical prote	1262	58.5	6.4	1049	1	S51784	toxin III - Actino
1190	58.5	6.4	370	1	B71937	probable membrane-	1263	58.5	6.4	1052	1	B49219	toxin III - Actino
1191	58.5	6.4	377	2	AR1991	hypothetical prote	1264	58.5	6.4	1055	1	GMLJ5T	HIV-1 retropepsin
1192	58.5	6.4	382	2	T22798	hypothetical prote	1265	58.5	6.4	1064	1	S57450	protein-tyrosine k
1193	58.5	6.4	385	2	AH2200	two-component hydr	1266	58.5	6.4	1077	2	T01474	hypothetical prote
1194	58.5	6.4	389	2	A85759	probable heat shoc	1267	58.5	6.4	1102	2	T02782	probable relaxase
1195	58.5	6.4	389	2	E90860	probable heat shoc	1268	58.5	6.4	1128	2	AH1949	hypothetical prote
1196	58.5	6.4	389	2	C64876	ycjM protein precu	1269	58.5	6.4	1132	2	T00259	hypothetical prote
1197	58.5	6.4	394	2	T37520	arginase family pr	1270	58.5	6.4	1144	1	A39833	adenylate cyclase

1271	58.5	6.4	1188	2	F64367	pyruvate, water, di	1344	58	6.4	498	2	T23525	hypothetical prote
1272	58.5	6.4	1273	2	T34558	hypothetical prote	1345	58	6.4	511	2	T27716	hypothetical prote
1273	58.5	6.4	1274	2	T02635	DI protein homolog	1346	58	6.4	530	2	A35144	hypothetical prote
1274	58.5	6.4	1300	2	T18364	ro-3 protein - Neu	1347	58	6.4	530	2	T41865	G664/67 EFP or f128
1275	58.5	6.4	1319	2	S75705	hypothetical prote	1348	58	6.4	538	2	T27156	hypothetical prote
1276	58.5	6.4	1343	2	T20718	hypothetical prote	1349	58	6.4	550	2	F86127	hypothetical prote
1277	58.5	6.4	1353	2	JC4279	adenylate cyclase	1350	58	6.4	550	2	B91286	hypothetical prote
1278	58.5	6.4	1475	2	T33318	hypothetical prote	1351	58	6.4	551	2	C84549	probable membrane
1279	58.5	6.4	1501	2	S57198	multidrug resistan	1352	58	6.4	573	2	S49266	beta-fructofuranos
1280	58.5	6.4	1608	2	T17201	adenylate cyclase	1353	58	6.4	576	2	C86893	cell division regu
1281	58.5	6.4	1711	1	A47392	chomodomain-helic	1354	58	6.4	577	2	T47838	beta-glucosidase-1
1282	58.5	6.4	1932	2	T25525	hypothetical prote	1355	58	6.4	581	2	T38864	probable regulator
1283	58.5	6.4	2541	2	S11661	hypothetical prote	1356	58	6.4	585	1	A24168	involucrin - human
1284	58	6.4	154	2	B71263	calin - mouse	1357	58	6.4	588	2	T48009	PECTINESTERASE-lik
1285	58	6.4	155	2	AD2524	hypothetical prote	1358	58	6.4	594	2	T04545	protein c8/ch-42,
1286	58	6.4	172	2	A80293	hypothetical prote	1359	58	6.4	607	2	E70165	hypothetical prote
1287	58	6.4	178	2	F83664	transcription anti	1360	58	6.4	608	2	A72213	1-deoxyxylulose-5-
1288	58	6.4	206	2	T14330	homeotic protein -	1361	58	6.4	608	2	D87912	protein B0205.3 [i
1289	58	6.4	207	2	D72215	hypothetical prote	1362	58	6.4	615	2	T15575	hypothetical prote
1290	58	6.4	228	2	T47847	hypothetical prote	1363	58	6.4	635	2	F90551	lipoprotein (impor
1291	58	6.4	253	2	E69098	phosphate transpor	1364	58	6.4	647	1	F58353	LIM protein kinase
1292	58	6.4	258	2	S25622	coat protein - cas	1365	58	6.4	659	2	D84286	3-hydroxyacyl-CoA
1293	58	6.4	258	2	S25623	coat protein - cas	1366	58	6.4	663	2	B70460	exonuclease ABC c
1294	58	6.4	260	2	T12446	MADH2 dehydrogenas	1367	58	6.4	686	2	G85940	type III secretion
1295	58	6.4	260	2	T12441	MADH2 dehydrogenas	1368	58	6.4	686	2	C91095	type III secretion
1296	58	6.4	260	2	T12447	MADH2 dehydrogenas	1369	58	6.4	695	1	ORHUP7	follicleotropin recept
1297	58	6.4	260	2	T12432	MADH2 dehydrogenas	1370	58	6.4	705	2	T20278	hypothetical prote
1298	58	6.4	261	2	S52609	hypothetical prote	1371	58	6.4	714	2	H82242	phosphate acetylitr
1299	58	6.4	264	2	F71466	hypothetical prote	1372	58	6.4	723	2	A49613	enoyl-CoA hydratase
1300	58	6.4	266	2	I49114	hypothetical prote	1373	58	6.4	741	2	T13776	MADH2 dehydrogenas
1301	58	6.4	266	2	I49051	Ly-49H - mouse	1374	58	6.4	741	2	T13247	MADH2 dehydrogenas
1302	58	6.4	266	2	A70345	Ly-49F-GF antigen	1375	58	6.4	742	2	T12422	propionate convert
1303	58	6.4	277	2	AD3358	2-dehydro-3-deoxy-	1376	58	6.4	752	1	KXR1C1	hypothetical prote
1304	58	6.4	284	2	C64527	M protein - Helico	1377	58	6.4	757	2	T38124	RNA-directed RNA p
1305	58	6.4	291	2	T13619	hypothetical prote	1378	58	6.4	759	1	P31V61	RNA-directed RNA p
1306	58	6.4	298	2	S50735	beta-lactamase (EC	1379	58	6.4	759	1	P31VAK	RNA-directed RNA p
1307	58	6.4	307	1	PNBSL	hypothetical prote	1380	58	6.4	759	2	S04930	kinesin-like prote
1308	58	6.4	313	2	F70333	hypothetical prote	1381	58	6.4	777	2	C85065	hypothetical prote
1309	58	6.4	317	2	A10640	flagellar hook-ass	1382	58	6.4	781	2	F90547	hypothetical prote
1310	58	6.4	317	2	S10362	hook-associated pr	1383	58	6.4	784	2	A10513	organic solvent to
1311	58	6.4	318	2	A55356	conserved hypotnet	1384	58	6.4	820	2	T22172	hypothetical prote
1312	58	6.4	322	1	F64360	hypothetical prote	1385	58	6.4	830	2	E83031	conserved hypotnet
1313	58	6.4	328	2	H84548	hypothetical prote	1386	58	6.4	847	1	A53800	mixed-lineage prot
1314	58	6.4	333	2	D85068	DI23-like protein	1387	58	6.4	849	2	T19878	hypothetical prote
1315	58	6.4	342	2	B83272	conserved hypotnet	1388	58	6.4	860	2	T15778	hypothetical prote
1316	58	6.4	345	2	T02650	hypothetical prote	1389	58	6.4	899	2	B70119	preproteins translo
1317	58	6.4	361	2	T21740	hypothetical prote	1390	58	6.4	922	2	T20277	hypothetical prote
1318	58	6.4	361	2	T23732	glucosyl transfera	1391	58	6.4	926	2	H88226	protein G414.5 [i
1319	58	6.4	368	2	D70481	alpha-helical coil	1392	58	6.4	927	2	T47827	equimosa promoter
1320	58	6.4	371	2	A44122	hypothetical prote	1393	58	6.4	966	2	F84582	hypothetical prote
1321	58	6.4	373	2	S65176	Li-lactate dehydrog	1394	58	6.4	975	2	I59422	rac8 - rat (firgim
1322	58	6.4	381	2	G83050	lycopene cyclase -	1395	58	6.4	978	2	G75516	maltoooligosyltreha
1323	58	6.4	384	2	T51423	transposase ISCi31	1396	58	6.4	989	2	T11576	hypothetical prote
1324	58	6.4	386	2	S52981	probable Arac-fami	1397	58	6.4	1029	2	H96658	hypothetical prote
1325	58	6.4	395	2	C90328	hypothetical prote	1398	58	6.4	1030	2	A32612	spectrin alpha cha
1326	58	6.4	397	2	AG0490	argininosuccinate	1399	58	6.4	1039	2	S18199	myosin heavy chain
1327	58	6.4	402	2	E70656	hypothetical prote	1400	58	6.4	1061	2	A57620	steroid receptor c
1328	58	6.4	406	2	A34485	hypothetical prote	1401	58	6.4	1089	2	T30883	serine-repeat anti
1329	58	6.4	414	2	G31261	TYA protein - yeas	1402	58	6.4	1101	2	AB2461	hypothetical prote
1330	58	6.4	445	2	F97855	hypothetical prote	1403	58	6.4	1159	1	A44280	inner layer protei
1331	58	6.4	447	2	F85356	hypothetical prote	1404	58	6.4	1194	2	T37503	probable chromosom
1332	58	6.4	448	2	A83775	hypothetical prote	1405	58	6.4	1231	1	A48490	endo-,4-beta-xyla
1333	58	6.4	451	2	G82218	sensor histidine k	1406	58	6.4	1261	2	S75130	senosry transducti
1334	58	6.4	456	2	G81408	probable outer mem	1407	58	6.4	1300	2	A36502	insulin receptor-r
1335	58	6.4	461	2	B95887	probable aminotran	1408	58	6.4	1354	2	T28107	hypothetical prote
1336	58	6.4	463	2	T10015	hypothetical prote	1409	58	6.4	1354	2	T113930	tripeptidyl-peptid
1337	58	6.4	464	2	T15161	hypothetical prote	1410	58	6.4	1371	2	T29019	hypothetical prote
1338	58	6.4	475	1	RKCNTLU	ribulose-bisphosph	1411	58	6.4	1463	2	C86482	protein FSJ5.1 [im
1339	58	6.4	484	2	S35401	M1 protein precurs	1412	58	6.4	1475	2	F86339	protein P17L21.22
1340	58	6.4	484	2	S34978	benzaldehyde dehyd	1413	58	6.4	1566	2	S59393	probable membrane
1341	58	6.4	487	2	T747107	conserved hypotnet	1414	58	6.4	1612	2	S59969	DNA topoisomerase
1342	58	6.4	488	2	F86911	hypothetical prote	1415	58	6.4	1626	2	A39242	DNA topoisomerase
1343	58	6.4	493	2	T31794	hypothetical prote	1416	58	6.4	1803	2	S56894	TYB protein - yeas

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1419	58	6.4	1939	2	D97316
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1421	58	6.4	2091	2	A97077
1422	58	6.4	2427	2	T16613
1423	58	6.4	2925	2	T00133
1424	58	6.4	3144	2	A46068
1425	58	6.4	3746	1	YGPLV3
1426	58	6.4	3791	1	YGPLV8
1427	58	6.4	4056	2	H96599
1428	58	6.4	4351	2	T00252
1429	58	6.4	4869	2	S66572
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1431	57.5	6.3	148	1	GGHFG3
1432	57.5	6.3	151	1	B26092
1433	57.5	6.3	179	2	T22301
1434	57.5	6.3	190	2	F97301
1435	57.5	6.3	201	2	B88431
1436	57.5	6.3	205	2	B46177
1437	57.5	6.3	210	2	AH0234
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1439	57.5	6.3	210	2	B81788
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1441	57.5	6.3	211	2	E90174
1442	57.5	6.3	215	2	E72020
1443	57.5	6.3	215	2	D86605
1444	57.5	6.3	216	2	F84023
1445	57.5	6.3	226	2	AD1230
1446	57.5	6.3	228	2	H71682
1447	57.5	6.3	235	2	T47432
1448	57.5	6.3	239	2	C82870
1449	57.5	6.3	245	2	D1554
1450	57.5	6.3	248	2	T26412
1451	57.5	6.3	258	2	AF0499
1452	57.5	6.3	265	2	T24841
1453	57.5	6.3	275	2	S55978
1454	57.5	6.3	278	2	G82370
1455	57.5	6.3	282	1	F65061
1456	57.5	6.3	292	2	T34529
1457	57.5	6.3	293	2	D82557
1458	57.5	6.3	301	2	S57531
1459	57.5	6.3	309	2	F83044
1460	57.5	6.3	310	2	B64441
1461	57.5	6.3	316	2	A12423
1462	57.5	6.3	318	2	F87650
1463	57.5	6.3	327	2	T33541
1464	57.5	6.3	331	2	T05428
1465	57.5	6.3	342	2	T06272
1466	57.5	6.3	347	2	AC2456
1467	57.5	6.3	349	2	S40718
1468	57.5	6.3	352	1	CEBEPX
1469	57.5	6.3	352	2	G91167
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1471	57.5	6.3	354	2	A11976
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1476	57.5	6.3	367	2	H85160
1477	57.5	6.3	375	2	T10554
1478	57.5	6.3	376	2	T49255
1479	57.5	6.3	382	2	JL0053
1480	57.5	6.3	382	2	AJ7253
1481	57.5	6.3	394	2	T19571
1482	57.5	6.3	401	2	F86754
1483	57.5	6.3	408	1	A31888
1484	57.5	6.3	413	2	AC0882
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1486	57.5	6.3	427	2	B98125
1487	57.5	6.3	428	1	I64227
1488	57.5	6.3	433	2	T02655
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myosin heavy chain
myosin alpha heavy
probable S-layer p
ov1 protein - nem
hypothetical prote
hypothetical prote
RNA-directed RNA p
Huntington disease
alpha-aminoadipyl-
alpha-aminoadipyl-
protein F14J16.10
MEGF1 protein - ra
ryanodine receptor
ryanodine receptor
globin I1 - Atlan
myosin I2 catalyti
hypothetical prote
specialized sigma
protein M88.2 [imp
enhancer of split
probable two-compo
hypothetical prote
conserved hypotet
lipoprotein [limpor
superoxide dismuta
inorganic pyrophos
inorganic pyrophos
transcription regu
ABC transporter, A
H71682
hypothetical prote
hypothetical prote
probable adenylate
hypothetical prote
probable phosphate
hypothetical prote
hypothetical prote
shikimate 5-dehydr
hypothetical prote
hypothetical prote
ABC transporter su
transcription regu
nitrate-inducible
GMP synthase (glut
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farnesyl-pyrophosp
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cell division prot
cell division memb
cell division memb
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rap60 protein - Ba
protein kinase-lik
UDPglucose-hexose-
seum albumin - bu
hypothetical prote
probable pi2 prote
ribonucleoprotein
tRNA adenylityltras
peptidase, M16 fam
conserved hypotet
cysteine-tRNA ligase
hydroxymethylgluta
coenzyme F330 bnt

1490	57.5	6.3	437	2	S46613
1491	57.5	6.3	440	2	C34332
1492	57.5	6.3	444	2	A99496
1493	57.5	6.3	445	2	B83805
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1495	57.5	6.3	457	2	S52206
1496	57.5	6.3	458	2	B69528
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1499	57.5	6.3	463	2	B55508
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ALIGNMENTS

RESULT 1

JS0204
trophoblast interferon alpha precursor - sheep
N:Alternate names: antiluteolysin; trophoblast antiluteolytic protein; trophoblastic pro
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text change 09-Jul-2004
C:Accession: S03799; B61403; JS0204; A60947; A53867; S06221; S00306; A60857; A60936
R:Stewart, H.J.; Flint, A.P.F.; Lamming, G.E.; McCann, S.H.E.; Parkinson, T.J.
submitted to the EMBL Data Library, June 1988
A:Reference number: S03799
A:Accession: S03799
A:Molecule type: DNA
A:Residues: 1-195 <STE>
A:Cross-references: UNIPROT:P56828; UNIPROT:P56829; EMBL:X07920; NID:G1821; PIDN:CAA3075
R:Charlier, M.; Hue, D.; Boissard, M.; Martal, J.; Gaye, P.
Mol. Cell. Endocrinol. 76, 161-171, 1991
A:Title: Cloning and structural analysis of two distinct families of ovine interferon- α
A:Reference number: A61403; MUID:92324492; PMID:1820971
A:Accession: B61403
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-129, 'K', 131-195 <CHA>
R:Charlier, M.; Hue, D.; Martal, J.; Gaye, P.
Gene 77, 341-348, 1989
A:Title: Cloning and expression of cDNA encoding ovine trophoblastin: its identity with
A:Reference number: JS0204; MUID:89326151; PMID:2753362
A:Accession: JS0204
A:Molecule type: mRNA
A:Residues: 1-195 <CHM>
A:Cross-references: GB:M26386; NID:G530199; PIDN:AAA31584.1; PID:G530200
A:Reference number: A60947; MUID:89351557; PMID:2475129
A:Accession: A60947
A:Experimental source: embryo
R:Stewart, H.J.; McCann, S.H.E.; Northrop, A.J.; Lamming, G.E.; Flint, A.P.F.
J. Mol. Endocrinol. 2, 65-70, 1989
A:Title: Sheep antiluteolytic interferon: cDNA sequence and analysis of mRNA levels.
A:Reference number: A60947; MUID:89351557; PMID:2475129
A:Accession: A60947
A:Molecule type: mRNA
A:Residues: 1-195 <ST3>
R:Stewart, H.J.; Flint, A.P.F.; Lamming, G.E.; McCann, S.H.E.; Parkinson, T.J.
J. Reprod. Fertil. Suppl. 37, 127-138, 1989
A:Title: Antiluteolytic effects of blastocyst-secreted interferon investigated in vitro
A:Reference number: A53867; MUID:90040431; PMID:2530342
A:Accession: A53867
A:Molecule type: mRNA
A:Residues: 1-195 <ST4>
R:Imakawa, K.; Anthony, R.V.; Kazemi, M.; Marrocci, K.R.; Polites, H.G.; Roberts, R.M.
Nature 330, 377-379, 1987
A:Title: Interferon-like sequence of ovine trophoblast protein secreted by embryonic tro
A:Reference number: S06221; MUID:88065855; PMID:2446135
A:Accession: S06221
A:Molecule type: mRNA
A:Residues: 1-27, 'RK', 30-105, 'E', 107-195 <IMA>
A:Cross-references: GB:Y00287; NID:G1357; PIDN:CAA6836.1; PID:G1358
R:Charligny, G.; Reinaud, P.; Hue, J.C.; Guillomoc, M.; Charlier, M.; Pernollet, J.C.;
FEBS Lett. 228, 12-16, 1988
A:Title: High homology between a trophoblastic protein (trophoblastin) isolated from ovi
A:Reference number: S00306; MUID:88137579; PMID:33254170

Db 84 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Db 144 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 195

RESULT 5

61578 trophoblast protein 1 (clone SPW49) - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 17-Mar-1999

C/Accession: A61578

R/Accession: A61578

R/Accession: A61578

R/Accession: A61578

A:Residues: 1-172 <MAT>

A:Superfamily: Interferon alpha

C/Keywords: glycoprotein, pregnancy maintenance

F/78/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.4%; Score 847; DB 2; Length 172;

Best Local Similarity 93.0%; Pred. No. 2.2e-70;

Matches 160; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKLTDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 60

Db 1 CYLSRKMLDARENKLTDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 60

Qy 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 120

Db 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 120

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Db 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

RESULT 6

146272 trophoblast interferon - goat

C/Species: Capra aegagrus hircus (domestic goat)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C/Accession: I46272

R/Accession: I46272

R/Accession: I46272

A:Residues: 1-195 <LEA>

A:Superfamily: Interferon alpha

Query Match 93.3%; Score 846; DB 2; Length 195;

Best Local Similarity 93.6%; Pred. No. 3.2e-70;

Matches 161; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKLTDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 60

Db 24 CYLSRKMLDARENKLTDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 83

Qy 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 120

Db 84 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Db 144 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 195

RESULT 7

61455 trophoblast protein 1 precursor - sheep

N/Alternate names: Interferon

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004

C/Accession: A61455; S12624

R/Accession: A61455

R/Accession: A61455

A:Residues: 1-195 <ROB>

A:Superfamily: Interferon alpha

C/Keywords: glycoprotein, pregnancy maintenance

F/24-195/Product: trophoblast protein 1 #status predicted <MAT>

Query Match 92.8%; Score 842; DB 2; Length 195;

Best Local Similarity 93.0%; Pred. No. 7.4e-70;

Matches 160; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKLTDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 60

Db 24 CYLSRKMLDARENKLTDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 83

Qy 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 120

Db 84 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Db 144 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 195

RESULT 8

147067 trophoblast protein-1 - sheep

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004

C/Accession: I47067

R/Accession: I47067

R/Accession: I47067

A:Residues: 1-195 <NEP>

A:Superfamily: Interferon alpha

Query Match 88.9%; Score 806; DB 2; Length 195;

Best Local Similarity 89.5%; Pred. No. 1.5e-66;

Matches 154; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKLTDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 60

Db 24 CYLSRKMLDARENKLTDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAPFVLYEM 83

Qy 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 120

Db 84 LQGSFNLFTYTHSSAAMDITLLDQCTGLQQOQLDHLDTCRGVNGEEDSELGNMDDPIVTV 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Oy	1	CYLSRKMLDARENKILLDNRNRLSPHSCLODRKFGLPOEMWBGDOLOKQOAPRYLYEM	60
Db	24	CYLSRRLMLDARENIRLLDNRNRLSPHSCLODRKDFGLPOEWVBGDOLOEAOACFYLYEM	83
Oy	61	LQOSRNLFYERHSSAAMDPTTLLEQLCTGLQQQLBHLDTCRQOWNGEBDSSEJGNNDPIYTV	120
Db	84	LQOSRNLFYERHSSAAMWTTLLEQLCTGLQQQLBHLDTCRPVGKEKSEJGNNDPIYTV	143
Oy	121	KKYFGIIVDYLOEKGYSDCAMEIYRVENMRALLVSTTLQOKLTKMGCDLNSP	172
Db	144	KKYFGIHIDYLOEKGYSDCAMETVAVENMRALLTSSLQOKLTNTGGDLNSP	195

[illegible]

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RESULT 10
147098
trophoblast protein-1 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 16-Jul-1999
C:Accession: 147098
R:Lesman, D.W.; Roberts, R.M.
J. Interferon Res. 12, 1-11, 1992
A:Title: Genes for the trophoblast interferons in sheep, goat, and musk ox and distribution
A:Reference number: 146272; MUID:9242937; PMID:1374107
A:Accession: 147098
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-184 <LEA>
A:Cross-references: GB:WJ3242; NID:G166027; PID:AAA31574.1; PID:G166028
C:Genetics:
A:Gene: OIP-1
C:Superfamily: Interferon alpha

Query Match      82.1%; Score 745; DB 2; Length 184;
Best Local Similarity 88.8%; Pred. No. 5.3e-61;
Matches 142; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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[illegible]

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RESULT 11
A39505
trophoblast interferon 4 precursor (clone bFP4) - bovine
C.Species: Bos primigenius taurus (cattle)
C.Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004
C.Accession: A39505
R.Hansen, T.R.; Leeman, D.W.; Cross, J.C.; Mathialagan, N.; Bixby, J.A.; Roberts, R.M.
J. Biol. Chem. 266, 3060-3067, 1991
A.Title: The genes for the trophoblast interferons and the related interferon-alpha1 polypeptide
A.Reference number: A39505; MUID:9111606; PMID:1704373
A.Accession: A39505
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-195 <HAN>
A.Cross-References: UNIPROT:P15656; GB:M60908; NID:G163213; PIDN:AA62711.1; PID:G163214
A.Superfamily: Interferon alpha
F.1-33/Domains: signal sequence #status predicted <SIG>
F.24-195/Product: interferon alpha-II #status predicted <MAT>

```

Query Match	79.8%	Score 724	DB 2	Length 195
Best Local Similarity	80.7%	Pred. No. 4,7e-59		
Matches 138	Conservative 14	Mismatches 19	Indels 0	Gaps 0
QY	1	CYLSRKLMDARENLKTLDRMNLSPHSCIQDRKDFGLPEWMEGDQLQKQAPFLVYEM	60	
DB	24	CYLSENHMLGARENRLRLARNRNLSPHPCIQDRKDFGLPEWMEGNGQLQKQAPISVLHEM	83	
QY	61	LOQSRNLPFTHESSAAMDITLLLEQLCTGLQQLDLHDLTCRQVNGEEDSELGNMIPYIV	120	
DB	84	LOQCENLPFTHESSAAMNTLLLEQLCTGLQQLLEDLDAACGPVNGEKSDMGMRMGPILTV	143	
QY	121	KYYPGGIYIVLOEKGYSDCAMEIVRVEMNRALIVSTTLQKRLTKMGGLNS	171	
DB	144	KYYPGGIHYIVLEKEYSDCAMEIIRMEEMRALSSITLLQKRLRKMGGGLNS	194	

RESULT 12
 S23751
 trophoblast interferon type I precursor - bovine
 C|Species: Bos primigenius taurus (cattle)
 C|Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C|Accession: S23751
 R|Stewart, H.J.; McCann, S.H.E.; Flint, A.P.F.
 J|Mol. Endocrinol. 4, 275-282, 1990
 A|Title: Structure of an interferon- α h2a gene expressed in the bovine conceptus early
 A|Reference number: S23751, MUID:90334707, PMID:2378676
 A|Accession: S23751
 A|Status: preliminary
 A|Molecule type: DNA
 A|Residues: 1-195 <STE>
 A|Cross-references: UNIPROT:P15656; EMBL:X65539; NID:g765; PIDN:CAA46506.1; PID:g766
 C|Superfamily: interferon alpha

	Query Match	79.7%	Score 723	DB 2	Length 195
	Best Local Similarity	80.7%	Pred. No. 5,5e-53		
	Matches 138	Conservative 14	Mismatches 19	Indels 0	Gaps 0
Qy	1	CYLSRKLMDARENLKLLDRMNRLLSPHSCTQDRKDFGLPEQMEVGEQDQLQKDAAPFLVLEM	60		
Db	24	CYLSRSDHMGAEENRFLRLARMNRLLSPHPCLODRKDFGLPEQMEVGEQDQLQKDAAPFLVLEM	83		


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Db 24 CDSQNHVLFQTKNRLRLLGQWRRLSPFCLQDRKDFAPQEMVWEGDQLQEAQAISVLHEM 83
Oy 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHLDTCRGQVWGEEDSBLGNMDDIVTV 120
Db 84 LQGSFNLFTYTHSSAAMDITLLLEQLRTGLHQQLDLDLACLGQVWGEEDSALGRGTPTLAV 143
Oy 121 KKYPQGIYDYLQEKGYSDCAMEIVVEMMRALVTSTLQKRLTKMGDLSNP 172
Db 144 KRYFGIHVYLKEKGYSDCAMEIVRVEIMRSLSSSTLSQERLRMMDDGLSP 195

RESULT 17
Interferon omega - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: 147070
R:Leaman, D.W.; Roberts, R.M.
J: Interferon Res. 12, 1-11, 1992
A:Title: Genes for the trophoblast interferons in sheep, goat, and musk ox and distribut
A:Reference number: 146272; MUID:92242937; PMID:1374107
A:Accession: 147070
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <LEA>
A:Cross-references: UNIPROT:P28170; GB:M73245; NID:9165828; PIDN:AAA31507.1; PID:9165828
C:Genetic8:
A:Gene: OIFN-omega
C:Superfamily: Interferon alpha

Query Match 64.7%; Score 587; DB 2; Length 195;
Best Local Similarity 67.4%; Pred. No. 1.7e-46;
Matches 116; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

Oy 1 CYSRKLMLDARENLKLLDRMNRSLPHSCLODRKDFGLPQEMVWEGDQLQKQAFPVLYEM 60
Db 24 CDSQNHVLFQTKNRLRLLGQWRRLSPFCLQDRKDFAPQEMVWEGDQLQEAQAISVLHEM 83
Oy 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHLDTCRGQVWGEEDSBLGNMDDIVTV 120
Db 84 LQGSFNLFTYTHSSAAMDITLLLEQLRTGLHQQLDLDLACLGQVWGEEDSALGRGTPTLAV 143
Oy 121 KKYPQGIYDYLQEKGYSDCAMEIVVEMMRALVTSTLQKRLTKMGDLSNP 172
Db 144 KRYFGIHVYLKEKGYSDCAMEIVRVEIMRSLSSSTLSQERLRMMDDGLSP 195

RESULT 18
Interferon alpha - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: 146397
R:Nephew, K.P.; Whaley, A.E.; Christenson, R.K.; Imakawa, K.
BioJ. Reprod. 48, 768-778, 1993
A:Title: Differential expression of distinct mRNAs for ovine trophoblast protein-1 and r
A:Reference number: 146397; MUID:93250155; PMID:8485241
A:Accession: 146397
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <NEB>
A:Cross-references: UNIPROT:Q28561; EMBL:X59067; NID:g416541; PIDN:CAA41790.1; PID:g4165
C:Genetic8:
A:Gene: Amy 124
C:Superfamily: Interferon alpha

Query Match 64.5%; Score 585; DB 2; Length 195;
Best Local Similarity 66.9%; Pred. No. 2.6e-46;
Matches 115; Conservative 20; Mismatches 37; Indels 0; Gaps 0;

Oy 1 CYSRKLMLDARENLKLLDRMNRSLPHSCLODRKDFGLPQEMVWEGDQLQKQAFPVLYEM 60
Db 24 CDSQNHVLFQTKNRLRLLGQWRRLSPFCLQDRKDFAPQEMVWEGDQLQEAQAISVLHEM 83
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Db 24 CDSQNHVLFQTKNRLRLLGQWRRLSPFCLQDRKDFAPQEMVWEGDQLQEAQAISVLHEM 83
Oy 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHLDTCRGQVWGEEDSBLGNMDDIVTV 120
Db 84 LQGSFNLFTYTHSSAAMDITLLLEQLRTGLHQQLDLDLACLGQVWGEEDSALGRGTPTLAV 143
Oy 121 KKYPQGIYDYLQEKGYSDCAMEIVVEMMRALVTSTLQKRLTKMGDLSNP 172
Db 144 KRYFGIHVYLKEKGYSDCAMEIVRVEIMRSLSSSTLSQERLRMMDDGLSP 195

RESULT 19
Interferon alpha-II-1 precursor - bovine
N:Alternate names: BoIFN-alpha-II-1; BoIFN-omega-1
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: B23285
R:Capon, D.J.; Shepard, H.M.; Goeddel, D.V.
Mol. Cell. Biol. 5, 768-779, 1985
A:Title: Two distinct families of human and bovine interferon-alpha genes are coordinate
A:Reference number: A93070; MUID:65187974; PMID:2985969
A:Accession: B23285
A:Molecule type: DNA
A:Residues: 1-195 <CAP>
A:Cross-references: UNIPROT:P07352; GB:M11002; NID:g163177; PIDN:AAA30578.1; PID:g163178
A:Experimental source: pancreas
C:Comment: Viral infection induces coordinate expression of both alpha-I and alpha-II (on
C:Keywords: antiviral
C:Superfamily: Interferon alpha

Query Match 64.2%; Score 582; DB 1; Length 195;
Best Local Similarity 66.9%; Pred. No. 4.8e-46;
Matches 115; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

Oy 1 CYSRKLMLDARENLKLLDRMNRSLPHSCLODRKDFGLPQEMVWEGDQLQKQAFPVLYEM 60
Db 24 CDSQNHVLFQTKNRLRLLGQWRRLSPFCLQDRKDFAPQEMVWEGDQLQEAQAISVLHEM 83
Oy 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHLDTCRGQVWGEEDSBLGNMDDIVTV 120
Db 84 LQGSFNLFTYTHSSAAMDITLLLEQLRTGLHQQLDLDLACLGQVWGEEDSALGRGTPTLAV 143
Oy 121 KKYPQGIYDYLQEKGYSDCAMEIVVEMMRALVTSTLQKRLTKMGDLSNP 172
Db 144 KRYFGIHVYLQEKGYSDCAMEIVRVEIMRSLSSSTLSQERLRMMDDGLSP 195

RESULT 20
Interferon alpha-II-5 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S23711
R:Mege, D.; Lefevre, F.; Labonnatiere, C.
J: Interferon Res. 11, 341-350, 1991
A:Title: The porcine family of interferon-omega: cloning, structural analysis, and funcn
A:Reference number: S23709; MUID:92193689; PMID:1800582
A:Accession: S23711
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <MEG>
A:Cross-references: UNIPROT:Q29085; EMBL:X57196; NID:g20066; PIDN:CAA40482.1; PID:g20067
C:Superfamily: Interferon alpha

Query Match 56.6%; Score 513.5; DB 2; Length 190;
Best Local Similarity 62.0%; Pred. No. 8.7e-40;
Matches 106; Conservative 24; Mismatches 36; Indels 5; Gaps 1;

Oy 1 CYSRKLMLDARENLKLLDRMNRSLPHSCLODRKDFGLPQEMVWEGDQLQKQAFPVLYEM 60
Db 24 CDSQNHVLFQTKNRLRLLGQWRRLSPFCLQDRKDFAPQEMVWEGDQLQEAQAISVLHEM 83
```


Biochim. Biophys. Acta 1089, 167-174, 1991
 A>Title: Human interferon omega-1: isolation of the gene, expression in Chinese hamster
 A:Reference number: S16174; MUID:91274345; PMID:1647209
 A:Accession: S16174
 A:Molecule type: DNA
 A:Residues: 1-195 <AD01>
 A:Cross-references: EMBL:X58822; NID:g32706; PIDN:CAA41626.1; PID:g32707
 A:Accession: S40306
 A:Molecule type: protein
 A:Residues: 22-23,'X',25-33 <AD02>
 R:Adolf, G.R.; Maurer-Fogy, I.; Kalener, I.; Cantelli, K.
 J. Biol. Chem. 265, 9290-9295, 1990
 A>Title: Purification and characterization of natural human interferon omegal. Two alter
 A:Reference number: A35299; MUID:90264422; PMID:1693148
 A:Accession: A35299
 A:Molecule type: protein
 A:Residues: 22-33 <ADO>
 A:Note: experimental source: leukocytes
 A:Note: evidence for two amino terminals, glycosylation
 R:Shiono, H.; Kono, K.; Koga, J.; Hayashi, S.; Matsuo, A.; Hiratani, H.
 Biochem. Biophys. Res. Commun. 168, 16-21, 1990
 A>Title: Existence and unique N-terminal sequence of alpha II (omega) interferon in natu
 A:Reference number: A34618; MUID:90262653; PMID:2156314
 A:Accession: A34618
 A:Molecule type: protein
 A:Residues: 22-33 <SH1>
 A:Note: evidence for two amino terminals
 A:Comment: Viral infection induces coordinate expression of both alpha-1 and omega-1 gen
 C:Genetics:
 A:Gene: GDB:1FNM1
 A:Cross-references: GDB:134207; OMIM:147553
 A:Map position: 9p22-9p22
 C:Superfamily: Interferon alpha
 C:Keywords: antiviral; cytokine; glycoprotein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-195/Product: interferon omega-1, long form #status experimental <MAT1>
 F:24-195/Product: interferon omega-1 #status experimental <MAT2>
 F:24-122,52-162/Disulfide bonds: #status predicted
 F:101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.1%; Score 473; DB 1; Length 195;
 Best Local Similarity 55.6%; Pred. No. 4,6e-36;
 Matches 95; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

QY 1 CYLSRKLMLDARENKILDRMNRSLSPHSCLDRKDFGIPQEMVEBDDQLQKQAFVLYEM 60
 DB 24 CDLPQNHLLSNTLVLLHQMRISPFCLDRDRFRFRQEMVKGSQLQXAHWSVLHEM 83
 QY 61 LQGSFNLFTYTHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRQVNGEEDSELGNDDPIVTV 120
 DB 84 LQQLFSLFHTTERRSSAAMWTLTLDQHTGTGHOOLQHLFTCLLQVVGEGESAGAISSPALT 143
 QY 121 KKYFGCIVDYLOEKGYSDCAWEIVVEMRALTVTTLQKLTGKGGLNS 171
 DB 144 RRYFGIVLYLEKKYSDCAWEIVVEMRALTVTTLQKLTGKGGLNS 194

RESULT 25
 S23710
 Interferon alpha-II-4 precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S23710
 R:Mege, D.; Lefevre, F.; Labonnardiere, C.
 J. Interferon Res. 11, 341-350, 1991
 A>Title: The porcine family of interferon-omega: cloning, structural analysis, and funct
 A:Reference number: S23709; MUID:92193689; PMID:1800582
 A:Accession: S23710
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-179 <MEG>
 A:Cross-references: UNIPROT:Q29084; EMBL:X57195; NID:g2064; PIDN:CAA40481.1; PID:g2065
 C:Superfamily: Interferon alpha

Query Match	51.8%	Score 469.5	DB 2	Length 179
Best Local Similarity	59.0%	Pred. No. 8.7e-36		
Matches	95	Conservative 26	Mismatches 35	Indels 5
			Gaps 1	
QY	1	CYLSRKMLDARENIKLDNRNRLSPHSCLDDRKDFGIPQEVVEDQLOKQAPVLYEM	60	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
DB	24	CDLFQNHVHVRKKNLVLRQMRRLSPSCFLCDKDRKDFGIPQEVVEDQLOKQALISLVHEM	83	
QY	61	LQGSFNLFYTHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRQGVNGEEDSELGNMPTIVT	120	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
DB	84	LQGFLLHTERRSSAAMDSTLLDKLCSGLHOLEDLLEBCLVQVHGEOASALE-----MAV	138	
QY	121	KKYFGIYDYLOEKGYSDCAWEIVRVEMRRLVYSTTLQKR	161	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
DB	139	KRYEGIHLYLKEKKYSDCAWEIVRVETMRRLISPMNQER	179	

RESULT 26
151970
interferon precursor - human
C.Species: Homo sapiens (man)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C.Accession: 151970
R.Savelliev, V.I.; Zlochevsky, M.L.; Sorokin, A.V.; Naroditskaya, V.A.; Bolotin, A.P.; D
Antibiot. Med. Biotechnol. 31, 592-596, 1986
A.Title: [Cloning and the determination of the nucleotide sequences in 2 genes of human
A.Reference number: 151970; MUID:87024453; PMID:3767336
A.Accession: 151970
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-189 <RES>
A.Cross-references: GB:M8289; NID:G186407; PIDN:AAA59165.1; PID:G186408
C.Genetics:
A.Gene: IFNA
C.Superfamily: interferon alpha

Query Match	50.1%	Score 454	DB 2	Length 189
Best Local Similarity	56.7%	Pred. No. 2.4e-34		
Matches	93	Conservative 25	Mismatches 46	Indels 0
			Gaps 0	
QY	1	CYLSRKMLDARENIKLDIRNNRSLSPHSCLODRKDFGLPQEMVEEDLOKQDAFVLYEM	60	
DB	24	CDLPQTHSLGNRRALILAQMGRISSPSCLDKDRHDFGLPQEPFDGNOQKQAIIVLYEM	83	
QY	61	LQGSFNLFYTEHSSAAMDITLLEQLCTGLAQQLDLDTCRQGVMEEDSELGNDPIVTV	120	
DB	84	IQQTFNLPSTEDSSAAEQGLLEKFKSTELYQQLNVLACVLIQEVGMEEPTPLNEDSILAV	143	
QY	121	KKYFGIGIYDIQEKGYSDCAWEIYRVEMRRALVYSTTLQKSLTK	164	
DB	144	KYFQRIILYLTKEKGYSDCAWEIYRAEIMRSLSEFTINQKSLRR	187	

RESULT 27
 156314
 Interferon-alpha - human (fragment)
 C|Species: Homo sapiens (man)
 C|Date: 02-Jul-1996 #sequence
 C|Accession: 156314
 R|lund, B.; von Gabain, A.; Edlund, T.; Ny, T.; Lundgren, E.
 J. Interferon Res. 5, 229-238, 1985
 A|Title: Differential expression of interferon genes in a substrain of Namalwa cells.
 A|Reference number: 156314; MUID:85235859; PMID:4008999
 A|Accession: 156314
 A|Status: preliminary; translated from GB/EMBL/DBJ
 A|Molecule type: mRNA
 A|Residues: 1-176 <RBS>
 A|Cross-references: UNIPROT:P01571; GB:M71246; NID:G184572; PIDN:AAA52713.1; PID:G184572
 C|Genetics:
 A|Gene: IFNA
 C|Superfamily: Interferon alpha

Oy 71 EHSSAAMDITLLEOCTGLQOQDLHLDTCRQVWGEEDSELGNDMPITVKKYFGCIYD 130
 Db 94 ARSSAAMNLTLEELHTLHQQLOGLCTLVQAMGEESVLTADSPITMLKKYFQIRILY 153
 Oy 131 LOEKGYSDCAMEIYVENMRALTSTTLOKRLTKKGGDLNSP 172
 Db 154 LDEKHGSCAMEIYVEMIRAFSSRADIQESLRSDGDLAS 195

RESULT 34

Interferon alpha-I-4b precursor - human

N:Alternate names: HuIFN-alpha-I-4b; type I interferon

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C:Accession: E23753

R:Henico, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov

J. Mol. Biol. 185, 227-260, 1985

A:Title: Structural relationship of human interferon alpha genes and pseudogenes.

A:Reference number: A92916; MUID:86037205; PMID:4057246

A:Accession: E23753

A:Molecule type: DNA

A:Residues: 1-189 <HFN>

A:Cross-references: UNIPROT:P05014; GB:X02955; NID:932656; PIDN:CAA26701.1; PID:g758078

C:Gene: GDB:IFN1@

A:Cross-references: GDB:119328; OMIM:147660

A:Map position: 9p22-9p22

C:Superfamily: Interferon alpha

C:Keywords: antiviral

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-189/Product: Interferon alpha-I-4b #status predicted <MAT>

F:24-122,52-162/Diulfide bonds: #status predicted

Query Match 47.3%; Score 429; DB 1; Length 189;

Best Local Similarity 54.3%; Pred. No. 4,8e-32;

Matches 89; Conservative 25; Mismatches 50; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKLLDRNNRSLSPHSCLODRKDFGLPQEMVSGDOLQKQAPVLYEM 60
 Db 24 CDLPQTHSLGNRRALLILGQGRISPHSCLODRHDFRIPQEPFQNOFOKAQALSVLHEM 83
 Oy 61 LOQSFNLFYTEHSSAAMDITLLEOCTGLQOQDLHLDTCRQVWGEEDSELGNDMPITV 120
 Db 84 IQQFNLFTSTEDSSAAMGOSLLEKFTSTLYQQLNDLEACVIOEVGVETPLMNDSTILAV 143
 Oy 121 KKYFGIYDYOEKGYSDCAMEIYVENMRALTSTTLOKRLTK 164
 Db 144 RKYFORITLYLERKYSFCAMEIVRAEIMRSLSTFSTNLOKRLR 187

RESULT 35

Interferon alpha-5 precursor - human

C:Species: Homo sapiens (man)

C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: A60937; A01830

R:Bartholomew, C.; Windaas, J.D.

J. Interferon Res. 9, 407-417, 1989

A:Title: Identification of a functional allele of a human interferon-alpha gene previous

A:Reference number: A60937; MUID:89328015; PMID:2526839

A:Accession: A60937

A:Molecule type: DNA

A:Residues: 1-189 <BAR>

A:Cross-references: UNIPROT:P01566

A>Note: This genomic sequence, SMITII.1A, encodes a functional allele for alpha interfer

ence and is a pseudogene

R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg

Nature 290, 20-26, 1981

A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.

A:Reference number: A93249; MUID:81148795; PMID:6163083

A:Accession: A01830

A:Molecule type: mRNA

A:Residues: 1-189 <GOE>
 A:Cross-references: GB:V00551; GB:J00209; NID:932748; PIDN:CAA23812.1; PID:g32749

A>Note: eight clones of interferon alpha clones were identified; this sequence is deriv

C:Gene: GDB:IFNA5

A:Cross-references: GDB:136362; OMIM:147565

A:Map position: 9p22-9p22

C:Superfamily: Interferon alpha

C:Keywords: Leukocyte

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-189/Product: Interferon alpha-5 #status predicted <MAT>

F:24-122,52-162/Diulfide bonds: #status predicted

Query Match 47.3%; Score 429; DB 1; Length 189;

Best Local Similarity 54.3%; Pred. No. 4,8e-32;

Matches 89; Conservative 26; Mismatches 49; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKLLDRNNRSLSPHSCLODRKDFGLPQEMVSGDOLQKQAPVLYEM 60
 Db 24 CDLPQTHSLGNRRALLILGQGRISPHSCLODRHDFRIPQEPFQNOFOKAQALSVLHEM 83
 Oy 61 LOQSFNLFYTEHSSAAMDITLLEOCTGLQOQDLHLDTCRQVWGEEDSELGNDMPITV 120
 Db 84 IQQFNLFTSTEDSSAAMGOSLLEKFTSTLYQQLNDLEACVIOEVGVETPLMNDSTILAV 143
 Oy 121 KKYFGIYDYOEKGYSDCAMEIYVENMRALTSTTLOKRLTK 164
 Db 144 RKYFORITLYLERKYSFCAMEIVRAEIMRSLSTFSTNLOKRLR 187

RESULT 36

Interferon alpha-1 precursor - human

N:Alternate names: Interferon alpha-13; Interferon alpha-D; Interferon alpha-I-1

C:Species: Homo sapiens (man)

C:Date: 22-May-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: C23285; A91467; A93226; A93249; I56213; S43715; S41196; A01826

R:Capon, D.J.; Shepard, H.W.; Goeddel, D.V.

Mol. Cell. Biol. 5, 768-779, 1985

A:Title: Two distinct families of human and bovine interferon-alpha genes are coordinate

A:Reference number: A93070; MUID:85187974; PMID:2985969

A:Accession: C23285

A:Molecule type: DNA

A:Residues: 1-189 <CAP>

A:Cross-references: UNIPROT:P01562

R:Mantel, N.; Schwarzeisen, M.; Streuli, M.; Panem, S.; Nagata, S.; Weissmann, C.

Gene 10, 1-10, 1980

A:Title: The nucleotide sequence of a cloned human leukocyte interferon cDNA.

A:Reference number: A91467; MUID:81005094; PMID:6157600

A:Accession: A91467

A:Molecule type: mRNA

A:Residues: 1-189 <MAN>

A:Cross-references: GB:V00537; NID:932711; PIDN:CAA23798.1; PID:g32712

R:Taniuchi, T.; Mantel, N.; Schwarzeisen, M.; Nagata, S.; Muramatsu, M.; Weissmann, C.

Nature 285, 547-549, 1980

A:Title: Human leukocyte and fibroblast interferons are structurally related.

A:Reference number: A93226; MUID:80254543; PMID:6157095

A:Accession: A93226

A:Molecule type: mRNA

A:Residues: 1-189 <TAN>

R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg

Nature 290, 20-26, 1981

A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.

A:Reference number: A93249; MUID:81148795; PMID:6163083

A:Accession: A93249

A:Molecule type: mRNA

A:Residues: 1-136, 'V', 138-189 <GOE>

A:Cross-references: GB:V00538; NID:932713; PIDN:CAA23799.1; PID:g32714

A>Note: eight clones of interferon alpha clones were identified; this sequence is deriv

R:Weber, H.; Weissmann, C.

Nucleic Acids Res. 11, 5661-5669, 1983

A:Title: Formation of genes coding for hybrid proteins by recombination between related,

A:Accession: I58213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 24-189 <RES>
A:Cross-references: GB:M29884; NID:G184583; PIDN:AA52714.1; PID:G386794
R:Hencho, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A:Title: Structural relationship of human interferon alpha genes and pseudogenes.
A:Reference number: A92916; MUID:86037205; PMID:6057246
A:Accession: S43715
A:Molecule type: DNA
A:Residues: 1-189 <HEN>
A:Cross-references: EMBL:X75934
R:Roelofs, N.
submitted to the EMBL Data Library, December 1993
A:Reference number: S41196
A:Accession: S41196
A:Molecule type: DNA
A:Residues: 1-9, 'A', 11-189 <ROS>
A:Cross-references: EMBL:X75934; NID:G439666; PIDN:CA53538.1; PID:G439667
C:Genetics:
A:Gene: GDB:IFNA1
A:Cross-references: GDB:136353; OMIM:147660
A:Map position: 9p22-9p22
C:Superfamily: interferon alpha
C:Keywords: antiviral; cytokine; leukocyte
F.1-23/Domains: signal sequence #status predicted <SIG>
F.24-189/Product: interferon alpha-1 #status predicted <MAT>
F.24-122,52-162/Diulide bonds: #status predicted

Query Match 47.2%; Score 428; DB 1; Length 189;
Best Local Similarity 53.9%; Pred. No. 5.9e-32;
Matches 90; Conservative 24; Mismatches 47; Indels 6; Gaps 2;

Qy 1 CYLSRKMLDARENKILDRNRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 60
Db 24 CDLPETHSLDRNRRLTLMIAQMSRISPSCLMDRHFPGPEEPGNGQFOKAPATSVLHEL 83
Qy 61 LQGSFNLFTYEHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRGQVWGEE--DSELGNDPI 117
Db 84 IQQIFNLFTTQSSAAMEDLLDKFCTELTQOQLNDLEAC--VMOEEVGETPLMNDASI 140

Qy 118 VTVKYPQGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLTK 164
Db 141 LAVKYPFRITLTYLEKKYSPCAMEVVAEIMRSLSSTNIOERLRR 187

RESULT 37
146975
Interferon-omega20 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I46975
R:Charlier, M.; L'Haridon, R.; Boissard, M.; Martal, J.; Gaye, P.
J. Interferon Res. 13, 313-322, 1993
A:Title: Cloning and structural analysis of four genes encoding interferon-omega in rabb
A:Reference number: I46972; MUID:94132653; PMID:8301151
A:Accession: I46975
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <CHA>
A:Cross-references: UNIPROT:Q28847; GB:S69129; NID:G545145; PIDN:AA60523.1; PID:G545146
C:Superfamily: interferon alpha

Query Match 47.1%; Score 427; DB 2; Length 195;
Best Local Similarity 54.0%; Pred. No. 7.6e-32;
Matches 87; Conservative 25; Mismatches 49; Indels 0; Gaps 0;

Qy 11 ARENKLIDRMNRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 70
Db 34 SRKTLVLDRNRRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 93
Qy 71 EHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRGQVWGEESELGNDPIVTVKYPQGIYD 130

Db 94 ARSSAANNLTLELHIALHQQQLQGLTCLVQAMGEEDSVLTADSPMLMKRYQRIRLY 153
Qy 131 LQEKGYSDCAMEIYRVEMRALTVSTTLQKRLTKMGDDLNS 171
Db 154 LDEKXSGCAMEIYRVEMIRAFSTADLQSLRSKDDLNS 194

RESULT 38
146972
Interferon-omega44 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I46972
R:Charlier, M.; L'Haridon, R.; Boissard, M.; Martal, J.; Gaye, P.
J. Interferon Res. 13, 313-322, 1993
A:Title: Cloning and structural analysis of four genes encoding interferon-omega in rabb
A:Reference number: I46972; MUID:94132653; PMID:8301151
A:Accession: I46972
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <CHA>
A:Cross-references: UNIPROT:Q28843; GB:S68997; NID:G545147; PIDN:AA60524.1; PID:G545148
C:Superfamily: interferon alpha

Query Match 47.0%; Score 426; DB 2; Length 195;
Best Local Similarity 52.0%; Pred. No. 9.3e-32;
Matches 89; Conservative 25; Mismatches 57; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKILDRNRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 60
Db 24 CDLPETHSLDRNRRLTLMIAQMSRISPSCLMDRHFPGPEEPGNGQFOKAPATSVLHEL 83
Qy 61 LQGSFNLFTYEHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRGQVWGEESELGNDPIVTV 120
Db 84 IQQIFNLFTTQSSAAMEDLLDKFCTELTQOQLNDLEAC--VMOEEVGETPLMNDASI 143
Qy 121 KKYFQGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLTKMGDDLNS 171
Db 144 KRYFQRIYLDKXSGCAMEIYRVEMIRAFSTADLQSLRSKDDLNS 194

RESULT 39
152347
Interferon alpha-M1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I52347
R:Linane, A.W.; Belharz, M.W.; McMullen, G.L.; Macreadie, I.G.; Murphy, M.; Nisbet, I.J.
Biochem. Int. 8, 725-732, 1984
A:Title: Nucleotide sequence and expression in E. coli of a human interferon-alpha gene
A:Reference number: I52347; MUID:84307815; PMID:6089830
A:Accession: I52347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189 <RES>
A:Cross-references: UNIPROT:P05014; GB:M27318; NID:G184617; PIDN:AA52726.1; PID:G306909
C:Genetics:
A:Gene: IFNA
C:Superfamily: interferon alpha

Query Match 46.9%; Score 425; DB 2; Length 189;
Best Local Similarity 54.3%; Pred. No. 1.1e-31;
Matches 89; Conservative 24; Mismatches 51; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKILDRNRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 60
Db 24 CDLPETHSLDRNRRLTLMIAQMSRISPSCLMDRHFPGPEEPGNGQFOKAPATSVLHEL 83
Qy 61 LQGSFNLFTYEHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRGQVWGEESELGNDPIVTV 120
Db 84 IQQIFNLFTTQSSAAMEDLLDKFCTELTQOQLNDLEACVIOEVGETPLMNDASI 143


```
QY      121 KKYFGIYDYLQEKGYSDCAWEIVREMMRALTVSTTLQKRLTK 164
      : ||| | | | | | | | | | | | | | | | | | | | |
DB      144 RKYFQRITLYLTEKKYSPCAWEIVRAEIMRSLSFSTNLQKRLRR 187
```

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RESULT 40
I46974
Interferon-omega45 - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C/Accession: I46974
R/Character: M.; L'Hardon, R.; Boissard, M.; Martal, J.; Gaye, P.
J. Interferon Res. 13, 313-322, 1993
A/Title: Cloning and structural analysis of four genes encoding interferon-omega in rabbit
A/Reference number: I46972; MUID:94132653; PMID:8301151
A/Accession: I46974
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-195 <CHA>
A/Cross-references: UNIPROT:Q28845; GB:S65000; NID:G545151; PIDN:AA60526.1; PID:G5451515
C/superfamily: Interferon alpha

```

[illegible]

RESULT 41
S70011
Interferon type I precursor - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S70011
R/Liu, L.; Leaman, D.W.; Bixby, J.A.; Roberts, R.M.
Biochim. Biophys. Acta 1294, 55-62, 1996
A/Title: A type I ovine interferon with limited similarity to IFN-alpha, IFN-omega and I
A/Reference number: S70011, MUID:9621986; PMID:8639714
A/Accession: S70011
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-195 <Liu>
A/Cross-References: UNIPROT:Q28545; EMBL:U26254; NID:9829612; PIDN:AA06828.1; PID:9829612
A/Superfamily: Interferon alpha

[illegible]

```

RESULT 42
I56313
Interferon alpha 21 - human
CISpecies: Homo sapiens (man)
CJDate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
CJAccession: I56313
R:Gron, E.; Berrin, V.M.; Jansone, I.; Tsaiminis, A.; Visnivesky, Y.; Apsalons, U.
J:Interferon Res. 4, 609-617, 1984
A>Title: Novel human leukocyte interferon subtype and structural comparison of alpha interc
A:Reference number: I56313; NCID:85056523; PMID:6548765
A:Accession: I56313
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-181 <RES>
A:Cross-references: UNIPROT:Q14608; GB:M28586; NID:G184636; PIDN:AAA36041.1; PID:G306912
C:Genetics:
A:Gene: GDB: IFNA21
A:Cross-references: GDB:136360; OMIM:147584
A:Map position: 9p22-9p22
C:Superfamily: Interferon alpha

```

Query Match	46.4%	Score 421	DB 2	Length 181
Best Local Similarity	52.4%	Pred. No. 2.4e-31		
Matches	86	Conservative 27	Mismatches 51	Indels 0
			Gaps	0

QY	1	CYLSRKLMLDARENLKILDRNNRRLSPHSCLDORKDFGLPQEMVEGDQLQDAAPVLYEM	60
DB	16	CDLPQTHSLGNRRALLLAQMGRIISFSCCLDRHDFGFPQEPGNGQKQKQALISVLHEM	75
QY	61	LQGSFNLFTYEHSSAAMDPTLLLEQLCTGLQOQLDHLDTCRQGVNGEEDSELGNDDPIATV	120
DB	76	IQGFNFNLSTKDSASATWQSLEKFPSTELNQLNDLEACVIOAEVGVEETPLMNVDSILAV	135
QY	121	KKYFQGIYDVLQEGKSYDCAMEIYRVEMRRLLATYSTLLQKRLTK	164
DB	136	KKYFQRLTLVLEKYSFPCAEVVRPAELIMRSFSLKFOEKLRR	179

```

RESULT 43
184464
Interferon-alpha-F - human
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I84464; I37583
R:Giren, E.Y.; Berzlin, V.M.; Timanis, A.Y.; Apselton, U.R.; Vishnevskii, Y.I.; Vansone, I.
.A.; Lozna, V.P.; Kavean, V.M.; Efimov, V.A.; Sveridov, E.D.
Dokl. Biochem. 269, 91-95, 1983
A:Title: A new type of leukocytic interferon.
A:Reference number: I37583
A:Accession: I84464
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189 <RES>
A:Cross-references: UNIPROT:P01568; GB:M12350; NID:g184598; PIDN:AA52718.1; PID:g306906
A:Accession: I37583
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189 <RES2>
A:Cross-references: EMBL:X00145; NID:g32724; PIDN:CAA24980.1; PID:g32725
C:Genetics:
A:Gene: IFNA
C:Superfamily: interferon alpha

Query Match      46.4%; Score 421; DB 2; Length 189;
Beet Local Similarity 52.4%; Pred. NO. 2.6e-31;
Matches 86; Conservative 27; Mismatches 51; Indels 0; Gaps 0;

```

[illegible]

Db 84 IQQFNLFTSKDSATWESQSLERKSTELNQNLDBACVIOEIVGEETPLMNVDSILAV 143
QY 121 KKVFQGIYDVLOEKGYSDCAMEIVRVEVMRALTVSTTLQKRLTK 164
Db 144 KKFQRTITLYTEKKYSPCAWEIVRAEIMRSFSLSKIPOERLKR 187

RESULT 44
E25843
Interferon alpha-F - human
N/Alternate names: human leukocyte interferon (IFN)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C/Accession: E25843
R/Ohara, O.; Terakoka, H.
FEBS Lett. 211, 78-82, 1987
A/Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel
A/Reference number: A91374; PMID:87105954; PMID:3803589
A/Accession: E25843
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-167 <OHA>
A/Cross-references: UNIPROT:Q14608
C/Superfamily: Interferon alpha

Query Match 46.2%; Score 419; DB 2; Length 167;
Best Local Similarity 51.8%; Pred. No. 3.4e-31;
Matches 85; Conservative 26; Mismatches 51; Indels 0; Gaps 0;

QY 1 CYLSRKLMIDARENKLLDRMNRSLSPHSCLODRKDFGLPOEMVSGDQLQKDAQFPVLYEM 60
Db 2 CDLPQTHSLGNRRALITLACWGRISPFSCLEKDRHDFGPFQEPFGDNGFQKAQAIISVLHEM 61

QY 61 LQGSFNLFTYHSSAAMDITLLEQLCTGLOQQLDHLDTCRGQVGEEDSELGNMDPIVTV 120
Db 62 IQQFNLFTSKDSATWESQSLERKSTELNQNLDBACVIOEIVGEETPLMNVDSILAV 121

QY 121 KKVFQGIYDVLOEKGYSDCAMEIVRVEVMRALTVSTTLQKRLTK 164
Db 122 KKFQRTITLYTEKKYSPCAWEIVRAEIMRSFSLSKIPOERLKR 165

RESULT 45
IVHUF
Interferon alpha-I-F precursor - human
N/Alternate names: HuIFN-alpha-I-F; LeIF F; type I interferon
C/Species: Homo sapiens (man)
C/Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C/Accession: A01832
R/Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg
Nature 290, 20-26, 1981
A/Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A/Reference number: A93249; MUID:81148795; PMID:6163083
A/Accession: A01832
A/Molecule type: mRNA
A/Residues: 1-189 <COGE>
A/Cross-references: UNIPROT:P01568; GB:V00540; GB:J00212; NID:G932716; PIDN:CAA23801.1; F
A/Note: eight classes of interferon alpha clones were identified, this sequence is deriv
C/Genetics:
A/Genes: GDB:IFN1@
A/Cross-references: GDB:119328; OMIM:147660
A/Map position: 9p22-9p22
C/Superfamily: interferon alpha
C/Keywords: antiviral
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-189/Product: interferon alpha-I-F #status predicted <MAT>
F/24-122,52-162/Disulfide bonds: #status predicted

Query Match 46.2%; Score 419; DB 1; Length 189;
Best Local Similarity 51.8%; Pred. No. 3.9e-31;
Matches 85; Conservative 28; Mismatches 51; Indels 0; Gaps 0;

QY 1 CYLSRKLMIDARENKLLDRMNRSLSPHSCLODRKDFGLPOEMVSGDQLQKDAQFPVLYEM 60

Db 24 CDLPQTHSLGNRRALITLACWGRISPFSCLEKDRHDFGPFQEPFGDNGFQKAQAIISVLHEM 83
QY 61 LQGSFNLFTYHSSAAMDITLLEQLCTGLOQQLDHLDTCRGQVGEEDSELGNMDPIVTV 120
Db 84 IQQFNLFTSKDSATWESQSLERKSTELNQNLDBACVIOEIVGEETPLMNVDSILAV 143

QY 121 KKVFQGIYDVLOEKGYSDCAMEIVRVEVMRALTVSTTLQKRLTK 164
Db 144 KKFQRTITLYTEKKYSPCAWEIVRAEIMRSFSLSKIPOERLKR 187

RESULT 46
IVHOA2
Interferon alpha-I-2 precursor - horse
N/Alternate names: EquIFN-alpha-I-2; type I interferon
C/Species: Equus caballus (domestic horse)
C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C/Accession: B24912
R/Himmler, A.; Hauptmann, R.; Adolf, G.R.; Sweetly, P.
DNA 5, 345-356, 1986
A/Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
A/Reference number: A90956; MUID:87053170; PMID:3022999
A/Accession: B24912
A/Molecule type: DNA
A/Residues: 1-184 <HIM>
A/Cross-references: UNIPROT:P05004; GB:M14541; NID:g164218; PIDN:AAA30950.1; PID:g164221
C/Superfamily: Interferon alpha

Query Match 45.0%; Score 408; DB 1; Length 184;
Best Local Similarity 51.2%; Pred. No. 3.9e-30;
Matches 82; Conservative 26; Mismatches 52; Indels 0; Gaps 0;

QY 1 CYLSRKLMIDARENKLLDRMNRSLSPHSCLODRKDFGLPOEMVSGDQLQKDAQFPVLYEM 60
Db 24 CDLPQTHSLGNRRALITLACWGRISPFSCLEKDRHDFGPFQEPFGDNGFQKAQAIISVLHEM 83

QY 61 LQGSFNLFTYHSSAAMDITLLEQLCTGLOQQLDHLDTCRGQVGEEDSELGNMDPIVTV 120
Db 84 IQQFNLFTSKDSATWESQSLERKSTELNQNLDBACVIOEIVGEETPLMNVDSILAV 143

QY 121 KKVFQGIYDVLOEKGYSDCAMEIVRVEVMRALTVSTTLQKRLTK 160
Db 144 RRYFORIALYLOEKYSPCAWEIVRAEIMRCFSSSTNLQ 183

RESULT 47
F25843
Interferon alpha-J - human
N/Alternate names: human leukocyte interferon (IFN)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 15-Jun-1996
C/Accession: F25843
R/Ohara, O.; Terakoka, H.
FEBS Lett. 211, 78-82, 1987
A/Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel
A/Reference number: A91374; MUID:87105954; PMID:3803589
A/Accession: F25843
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-167 <OHA>
C/Superfamily: Interferon alpha

Query Match 44.7%; Score 405; DB 2; Length 167;
Best Local Similarity 51.8%; Pred. No. 6.4e-30;
Matches 85; Conservative 26; Mismatches 53; Indels 0; Gaps 0;

QY 1 CYLSRKLMIDARENKLLDRMNRSLSPHSCLODRKDFGLPOEMVSGDQLQKDAQFPVLYEM 60

Db 2 CDLPQTHSLRNRRALLLAQMGRIISFSCLDNRHFRPPEEPDGHQFOKTOAISVLHEM 61
QY 61 LQGSFNLFTYTHSSAANDTTLLEOLCTGLQOQDLDTCRGVNGEEDSELGNMDDPIVTV 120
Db 62 IQQTFNLFSTEDSSAAWESQSLLEKFSFTELYOQLNDLEACVIOEAVGVEETPLMNEDEFLAV 121
QY 121 KKYFGQIYDYLQEGKGYSDCAMEIVRVMRRALTVSTTLQKRLTK 164
Db 122 RKYFQRITLVLMEKKYSPCAMEVVRRAEIMRSFSSTNLKGLRR 165

RESULT 48

IVHUA0

interferon alpha-7 precursor - human

N/Alternate names: Interferon alpha-J; Irf1 J

C/Species: Homo sapiens (man)

C/Date: 18-Aug-1992 #sequence_revision 18-Aug-1992 #text_change 09-Jul-2004

C/Accession: A01831; S43717

R/Unlrich, A.; Gray, A.; Goeddel, D.V.; Dull, T.J.

J. Mol. Biol. 156, 467-486, 1982

A/Title: Nucleotide sequence of a portion of human chromosome 9 containing a leukocyte 1

A/Reference number: A01831; MUID:83010248; PMID:6181262

A/Accession: A01831

A/Molecule type: DNA

A/Residues: 1-189 <H>

A/Cross-references: UNIPROT:P01567; GB:V00531; NID:932631; PIDN:CAA23792.1; PID:932632;

N/Note: This interferon is derived from a gene referred to as J by the authors

R/Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov

J. Mol. Biol. 185, 227-260, 1985

A/Title: Structural relationship of human interferon alpha genes and pseudogenes.

A/Reference number: A92916; MUID:86037205; PMID:4057246

A/Accession: S43717

A/Molecule type: DNA

A/Residues: 1-189 <H>

A/Cross-references: EMBL:X02960; NID:932665; PIDN:CAA26706.1; PID:9758081

C/Genetics:

A/Gene: GDB:IFNA7

A/Cross-references: GDB:136364; OMIM:147567

A/Map position: 9p22-9p22

C/Superfamily: Interferon alpha

C/Keywords: antiviral; cytokine; leukocyte

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-189/Product: interferon alpha-7 #status predicted <MAT>

F/24-122,52-162/Disulfide bonds: #status predicted

Query Match 44.7%; Score 405; DB 1; Length 189;
Best Local Similarity 51.8%; Pred. No. 7.5e-30;
Matches 85; Conservative 26; Mismatches 53; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLDNRNRLSPHSCLDRKDFGLPQEMVGGDLOKQDAFPVLYEM 60
Db 24 CDLPQTHSLRNRRALLLAQMGRIISFSCLDNRHFRPPEEPDGHQFOKTOAISVLHEM 83
QY 61 LQGSFNLFTYTHSSAANDTTLLEOLCTGLQOQDLDTCRGVNGEEDSELGNMDDPIVTV 120
Db 84 IQQTFNLFSTEDSSAAWESQSLLEKFSFTELYOQLNDLEACVIOEAVGVEETPLMNEDEFLAV 143
QY 121 KKYFGQIYDYLQEGKGYSDCAMEIVRVMRRALTVSTTLQKRLTK 164
Db 144 RKYFQRITLVLMEKKYSPCAMEVVRRAEIMRSFSSTNLKGLRR 187

RESULT 49

153102

interferon-alpha-J1 - human

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C/Accession: I53102

R/Cohen, S.; Velan, B.; Grosfeld, H.; Shalita, Z.; Leitner, M.; Shaffer, A.

Dev. Biol. Stand. 60, 111-122, 1985

A/Title: Cloning, expression and biological activity of a new variant of human interferon

A/Reference number: I53102; MUID:86005847; PMID:2995168

A/Accession: I53102

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-189 <RES>
A/Cross-references: UNIPROT:P01567; GB:M34913; NID:9184614; PIDN:AAA36039.1; PID:9184615
C/Superfamily: Interferon alpha

Query Match 44.5%; Score 404; DB 2; Length 189;
Best Local Similarity 51.8%; Pred. No. 9.3e-30;
Matches 85; Conservative 26; Mismatches 53; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLDNRNRLSPHSCLDRKDFGLPQEMVGGDLOKQDAFPVLYEM 60
Db 24 CDLPQTHSLRNRRALLLAQMGRIISFSCLDNRHFRPPEEPDGHQFOKTOAISVLHEM 83
QY 61 LQGSFNLFTYTHSSAANDTTLLEOLCTGLQOQDLDTCRGVNGEEDSELGNMDDPIVTV 120
Db 84 IQQTFNLFSTEDSSAAWESQSLLEKFSFTELYOQLNDLEACVIOEAVGVEETPLMNEDEFLAV 143
QY 121 KKYFGQIYDYLQEGKGYSDCAMEIVRVMRRALTVSTTLQKRLTK 164
Db 144 RKYFQRITLVLMEKKYSPCAMEVVRRAEIMRSFSSTNLKGLRR 187

RESULT 50

IVHUA1

interferon alpha-I-1 precursor - horse

N/Alternate names: EglfN-alpha-I-1; type I interferon

C/Species: Equus caballus (domestic horse)

C/Date: 28-Dec-1997 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C/Accession: A24912

R/Himmler, A.; Hauptmann, R.; Adolf, G.R.; Smetly, P.

DNA 5, 345-356, 1986

A/Title: Molecular cloning and expression in Escherichia coli of equine type I interferon

A/Reference number: A90956; MUID:87053170; PMID:3022999

A/Accession: A24912

A/Molecule type: DNA

A/Residues: 1-184 <H>

A/Cross-references: UNIPROT:P05003; GB:M14540; NID:9164226; PIDN:AAA30953.1; PID:9164227

C/Superfamily: Interferon alpha

C/Keywords: antiviral

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-184/Product: interferon alpha-I-1 #status predicted <MAT>

F/24-122,52-162/Disulfide bonds: #status predicted

Query Match 44.4%; Score 403; DB 1; Length 184;
Best Local Similarity 51.3%; Pred. No. 1.1e-29;
Matches 81; Conservative 26; Mismatches 51; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLDNRNRLSPHSCLDRKDFGLPQEMVGGDLOKQDAFPVLYEM 60
Db 24 CDLPQTHSLRNRRALLLAQMGRIISFSCLDNRHFRPPEEPDGHQFOKTOAISVLHEM 83
QY 61 LQGSFNLFTYTHSSAANDTTLLEOLCTGLQOQDLDTCRGVNGEEDSELGNMDDPIVTV 120
Db 84 IQQTFNLFSTEDSSAAWESQSLLEKFSFTELYOQLNDLEACVIOEAVGVEETPLMNEDEFLAV 143
QY 121 KKYFGQIYDYLQEGKGYSDCAMEIVRVMRRALTVSTTL 158
Db 144 RKYFQRITLVLMEKKYSPCAMEVVRRAEIMRSFSSTNL 181

Search completed: October 5, 2005, 10:38:41
Job time : 72 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 10:04:45 ; Search time 178 Seconds

(without alignments)
494.818 Million cell updates/sec

Title: US-10-694-247-2

Perfect score: 907
Sequence: 1 CYLSRKMLDARENLKILDR.....TSTTTLOKRLTKMGDLNSP 172Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summariesDatabase : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	907	100.0	195 1	INT1_SHEEP
2	900	99.2	195 1	INT2_SHEEP
3	888	97.9	172 1	INT3_SHEEP
4	881	97.1	195 1	INT4_SHEEP
5	880	97.0	195 1	INT7_SHEEP
6	877	96.7	195 1	INT5_SHEEP
7	868	95.7	195 1	INT9_SHEEP
8	865	95.4	195 1	INT8_SHEEP
9	846	93.3	195 1	INT_CAPI
10	842	92.8	195 1	INT6_SHEEP
11	830	91.5	195 2	OGUZ49
12	830	91.5	195 2	OGUZ50
13	816	90.0	172 2	OGRF28
14	806	88.9	195 1	INTA_SHEEP
15	804	88.6	195 1	OGUZ47
16	794	87.5	195 2	OGUZ43
17	786	86.7	195 2	OGUZ42
18	780	86.0	195 1	INT_OVIMO
19	778	85.8	195 1	INTB_SHEEP
20	726	80.0	195 1	INTI_SHEEP
21	721	79.5	172 2	INT2_BOVIN
22	719	79.3	172 2	OGMJ29
23	717	79.1	195 2	OGMYK6
24	707	77.9	172 1	INT3_BOVIN
25	702	77.4	195 2	OGGLT6
26	696	76.7	172 2	OGDUM3
27	693	76.4	195 2	OGGLU5
28	679	74.9	195 1	INT_GIRCA
29	653	72.0	195 1	INT_CEREL
30	609	67.1	195 1	INDI_HUMAN
31	608	67.0	195 2	Q7M2Y7

32	587	64.7	195 2	P28170	P28170 ovis aries
33	585	64.5	195 2	Q28561	Q28561 ovis aries
34	582	64.2	195 1	INOI_BOVIN	P07352 bos taurus
35	531	58.5	129 2	Q6SMQ8	Q6smq8 bos mutus g
36	513.5	56.6	190 2	Q29085	Q29085 sus scrofa
37	499	55.0	195 1	INO2_HORSE	P05002 equus caball
38	488.5	53.9	190 2	Q29098	Q29098 sus scrofa
39	473	52.1	195 1	INO1_HUMAN	P05000 homo sapien
40	469.5	51.8	179 2	Q29084	Q29084 sus scrofa
41	462	50.9	174 2	Q13168	Q13168 homo sapien
42	444	49.0	195 1	INO1_HORSE	P05001 equus caball
43	440	48.5	189 1	INAD_HUMAN	P01569 homo sapien
44	440	48.5	189 1	INAG_HUMAN	P01570 homo sapien
45	438	48.3	189 1	Q28562	Q28562 ovis aries
46	431	47.5	195 2	Q28844	Q28844 oryctolagus
47	430	47.4	195 2	INAA_HUMAN	P05014 homo sapien
48	429	47.3	189 1	INAA_HUMAN	P01566 homo sapien
49	429	47.3	189 1	OGUMJ3	OGumj3 homo sapien
50	428	47.2	166 2	INAI_HUMAN	P01562 homo sapien
51	428	47.2	189 1	Q14605	Q14605 homo sapien
52	428	47.2	189 2	Q28847	Q28847 oryctolagus
53	427	47.1	195 2	Q28843	Q28843 oryctolagus
54	426	47.0	195 2	Q95J78	Q95J78 saginus oe
55	425	46.9	189 2	Q28845	Q28845 oryctolagus
56	424	46.7	195 2	Q28545	Q28545 ovis aries
57	423	46.6	195 2	Q14608	Q14608 homo sapien
58	421	46.4	181 2	INAK_HUMAN	P01568 homo sapien
59	421	46.4	189 1	Q95J77	Q95J77 saginus oe
60	418	46.1	189 2	Q8WZ68	Q8WZ68 homo sapien
61	417	46.0	166 2	O7YRK9	O7Yrk9 sus scrofa
62	412	45.4	166 2	INA2_HORSE	P05004 equus caball
63	408	45.0	184 1	INA7_HUMAN	P01567 homo sapien
64	405	44.7	189 1	INA1_HORSE	P05003 equus caball
65	403	44.4	184 1	INA3_HORSE	P05005 equus caball
66	403	44.4	184 1	INA4_HORSE	P05006 equus caball
67	403	44.4	184 1	Q8MJT1	Q8mjt1 saimiri sci
68	400	44.1	174 2	Q68105	Q68105 sus scrofa
69	400	44.1	189 2	Q6VAB8	Q6Vab8 sus scrofa
70	399	44.0	189 1	Q86UP4	Q86up4 homo sapien
71	398	43.9	189 1	INA2_HUMAN	P01563 homo sapien
72	397.5	43.8	166 2	P792258	P792258 odocoileus
73	394.5	43.5	188 1	Q6QTF5	Q6qtf5 sus scrofa
74	394	43.4	189 2	Q14618	Q14618 homo sapien
75	394	43.4	189 2	INA8_HUMAN	P32881 homo sapien
76	392	43.2	189 1	INA1_PIG	P49879 sus scrofa
77	386	42.6	189 1	INA5_MOUSE	Q81062
78	384	42.3	189 1	Q80S04	Q80s04 mus musculu
79	384	42.3	189 2	Q81067	Q81067 mus musculu
80	384	42.0	189 2	Q6HOM6	Q6Hom6 bos sp. ifn
81	381	42.0	189 1	INA6_HUMAN	P05013 homo sapien
82	380	41.9	190 1	Q61719	Q61719 mus musculu
83	380	41.9	189 2	Q6HOM5	Q6Hom5 bos sp. ifn
84	379	41.8	166 2	Q6HOM6	Q6Hom6 bos sp. ifn
85	378	41.7	189 1	Q61718	Q61718 mus musculu
86	378	41.7	190 2	Q61719	Q61719 mus musculu
87	376	41.5	189 1	INA1_BOVIN	P07348 bos taurus
88	375	41.3	189 1	INA1_MOUSE	P01572 mus musculu
89	374	41.2	166 2	Q6HOM5	Q6Hom5 bos sp. ifn
90	374	41.2	190 1	INA7_MOUSE	P06799 mus musculu
91	372	41.0	190 1	INA2_MOUSE	P01573 mus musculu
92	372	40.9	166 2	Q7YRFO	Q7Yrf0 bos taurus
93	371	40.9	189 1	INAH_BOVIN	P49878 bos taurus
94	371	40.9	192 1	INAI_RAT	P05011 ratuus norv
95	370.5	40.8	154 2	Q6ONB6	Q6onb6 homo sapien
96	370	40.8	189 2	Q810G5	Q810G5 mus musculu
97	368	40.6	189 1	INAD_BOVIN	P05010 bos taurus
98	368	40.6	201 2	Q8R5K9	Q8R5K9 marmota mon
99	367	40.5	190 2	Q8R5K2	Q8R5K2 marmota mon
100	365.5	40.3	188 2	Q86316	Q86316 felis alive
101	365	40.2	190 2	Q8R5J2	Q8R5J2 marmota mon
102	365	40.2	190 2	Q64138	Q64138 cactocinae
103	364	40.1	190 2	Q61716	Q61716 mus musculu
104	364	40.1	190 2	Q61718	Q61718 mus musculu

105	364	40.1	190	2	0810G4	0810G4 mus musculus	178	197.5	21.8	182	2	0810G0	0810G0 mus musculus
106	363	40.0	190	2	08R5J4	08R5J4 marmota mon	179	197.5	21.8	182	2	08B0T1	08B0T1 mus musculus
107	362.5	40.0	188	2	08R5J5	08R5J5 felis silve	180	192.5	21.2	182	2	08C0T3	08C0T3 mus musculus
108	362	39.9	189	2	0808S5	0808S5 mus musculus	181	180.5	19.9	90	2	014645	014645 homo sapien
109	362	39.9	190	2	08R5U5	08R5U5 marmota mon	182	176	19.4	73	2	08HYG2	08HYG2 macropus eu
110	360	39.7	189	1	INAB_BOVIN	P05008 bos taurus	183	175	19.3	73	2	08HYG9	08HYG9 macropus eu
111	359	39.6	189	2	08M1L7	08M1L7 felis silve	184	172.5	19.0	184	1	INB_RAT	P70459 rattus norv
112	359	39.6	189	2	08M3I7	08M3I7 felis silve	185	170	18.7	73	2	08HYG5	08HYG5 macropus eu
113	359	39.6	189	2	08M3I8	08M3I8 felis silve	186	166	18.3	73	2	08HYG8	08HYG8 macropus eu
114	359	39.6	189	2	08M3I9	08M3I9 felis silve	187	164	18.1	73	2	08HYG6	08HYG6 macropus eu
115	359	39.6	189	2	08M3I0	08M3I0 felis silve	188	164	18.1	182	1	INB_MOUSE	08HYG6 macropus eu
116	358	39.5	166	2	Q7YRH9	Q7YRH9 bubalus bub	189	162	17.9	203	1	INFB_CHICK	P01575 mus musculus
117	358	39.5	166	2	Q7YRH9	Q7YRH9 bubalus bub	190	159	17.5	73	2	08HYG7	08HYG7 macropus eu
118	358	39.5	189	1	INAF_BOVIN	P49876 bos taurus	191	159	17.3	73	2	08HYH8	08HYH8 macropus eu
119	358	39.5	189	2	08M1T5	08M1T5 felis silve	192	157	17.3	180	2	Q70FG6	Q70FG6 fugu rubrip
120	358	39.5	190	2	08R5J3	08R5J3 marmota mon	193	156	17.2	180	2	063Z66	063Z66 fugu rubrip
121	358	39.5	190	2	08VHY8	08VHY8 marmota mon	194	155.5	17.1	82	2	Q912B3	Q912B3 mus musculus
122	357	39.4	189	1	INAG_BOVIN	P49877 bos taurus	195	155	17.1	73	2	08HYI4	08HYI4 macropus eu
123	357	39.4	189	2	0810G1	0810G1 mus musculus	196	151	16.6	73	2	08HYG3	08HYG3 macropus eu
124	357	39.4	191	2	06XL62	06XL62 mus musculus	197	149	16.4	73	2	08HYH3	08HYH3 macropus eu
125	356	39.3	189	2	08M1L3	08M1L3 felis silve	198	147	16.2	73	2	08HYF8	08HYF8 macropus eu
126	356	39.3	189	2	08M1L4	08M1L4 felis silve	199	147	16.2	73	2	08HYG0	08HYG0 macropus eu
127	356	39.3	189	2	0810G3	0810G3 mus musculus	200	147	16.2	199	2	Q7TSLO	Q7TSLO mus musculus
128	356	39.3	197	2	08R5J7	08R5J7 marmota mon	201	142	15.7	73	2	08HYI0	08HYI0 macropus eu
129	356	39.3	197	2	Q8VHZ1	Q8VHZ1 marmota mon	202	140	15.4	73	2	08HYH1	08HYH1 macropus eu
130	355	39.1	189	1	INAA_BOVIN	P05007 bos taurus	203	138	15.2	73	2	08HYH5	08HYH5 macropus eu
131	355	39.1	190	2	0810G6	0810G6 mus musculus	204	136.5	15.0	191	2	06CUZ2	06CUZ2 anser anser
132	355	39.1	190	2	Q9ESJ1	Q9ESJ1 marmota mon	205	134.5	14.8	193	1	INFI_CHICK	P42165 gallus gall
133	354	39.0	166	2	Q7YRL3	Q7YRL3 bos taurus	206	134.5	14.8	193	2	Q9PW16	Q9PW16 gallus gall
134	354	38.8	197	2	08VHZ0	Q8VHZ0 marmota mon	207	133.5	14.7	191	1	INP_ANAPL	P51526 anas platyr
135	351	38.7	189	1	INAC_BOVIN	P05009 bos taurus	208	133	14.7	73	2	08HYG1	08HYG1 macropus eu
136	350	38.6	197	2	08VHY9	08VHY9 marmota mon	209	133	14.7	73	2	08HYH2	08HYH2 macropus eu
137	349.5	38.5	194	2	08M1L6	08M1L6 felis silve	210	130	14.3	73	2	08HYH9	08HYH9 macropus eu
138	343	37.8	189	2	08R5J6	08R5J6 marmota mon	211	128.5	14.2	192	1	INP_MELGA	P51527 melagris g
139	342	37.7	189	1	INAB_MOUSE	P07350 mus musculus	212	127	14.0	73	2	08HYH0	08HYH0 macropus eu
140	340.5	37.5	194	1	INA_FELCA	P35849 felis silve	213	125.5	13.8	193	2	Q9PW15	Q9PW15 gallus gall
141	340.5	37.5	194	2	0863J1	0863J1 felis silve	214	124	13.7	73	2	08HYI3	08HYI3 macropus eu
142	340	37.5	189	1	INAB_MOUSE	P17660 mus musculus	215	123.5	13.6	193	1	INFI_CHICK	Q90872 gallus gall
143	335	36.9	136	1	0617I7	0617I7 mus musculus	216	123	13.6	73	2	08HYF9	08HYF9 macropus eu
144	331.5	36.5	186	1	INAA_MOUSE	P07351 mus musculus	217	119.5	13.2	176	2	Q7ZS24	Q7ZS24 tetradon n
145	329	36.3	183	2	Q7YRX8	Q7YRX8 macropus eu	218	113.5	12.5	72	2	08HXB0	08HXB0 cachygiossu
146	324	35.7	187	1	08R5U1	08R5U1 marmota mon	219	111	12.2	175	2	06XQG7	06XQG7 salmo salar
147	318	35.1	187	1	INAB_CANPA	Q97945 canis famill	220	110.5	12.2	72	2	016055	Q16055 homo sapien
148	317	35.0	187	2	0867A7	Q7YRX7 canis famill	221	110.5	12.2	72	2	08HYF5	08HYF5 cachygiossu
149	316	34.8	187	1	INAI_CANPA	P81255 canis famill	222	109.5	12.1	197	2	Q7SSP9	Q7SSP9 coturnix co
150	316	34.8	187	2	Q7SUT5	Q7SUT5 canis famill	223	109	12.0	175	2	06XQG6	Q6XQG6 salmo salar
151	314	34.6	190	2	Q91WX3	Q91WX3 sigmodon hi	224	107.5	11.9	72	2	016054	Q16054 homo sapien
152	313	34.5	187	2	Q7SUL7	Q7SUL7 canis famill	225	106	11.7	73	2	08HYH6	08HYH6 macropus eu
153	310	34.2	187	2	Q7SUL4	Q7SUL4 canis famill	226	104.5	11.5	72	2	Q9UNM4	Q9UNM4 homo sapien
154	301	33.2	183	2	Q7YRX7	Q7YRX7 macropus eu	227	103.5	11.4	68	2	08HYH7	08HYH7 macropus eu
155	294	32.4	108	2	Q9N1U6	Q9N1U6 equus cabal	228	103	11.4	73	2	08HYF3	08HYF3 cachygiossu
156	293	32.3	128	2	Q7TQ91	Q7TQ91 peromyscus	229	103	11.4	73	2	08HYF4	08HYF4 cachygiossu
157	290	32.0	208	2	086WN2	Q86WN2 homo sapien	230	100	11.0	73	2	08HYH4	08HYH4 macropus eu
158	287.5	31.7	186	1	INB2_BOVIN	P01576 bos taurus	231	99	10.9	73	2	08HYE2	08HYE2 cachygiossu
159	285	31.4	128	2	Q7TQ92	Q7TQ92 peromyscus	232	99	10.9	73	2	08HYI5	08HYI5 macropus eu
160	266.5	29.4	187	2	06XZW6	06XZW6 cachygiossu	233	97	10.7	73	2	08HYF6	08HYF6 cachygiossu
161	260	28.7	186	2	06B1Q4	06B1Q4 sus scrofa	234	97	10.7	73	2	08HYE7	08HYE7 macropus eu
162	257	28.3	186	1	INB_HORSE	P05012 equus cabal	235	96.5	10.6	133	2	Q70I18	Q70I18 oncorhynch
163	257	28.3	186	2	Q294I2	Q294I2 sus scrofa	236	94.5	10.4	68	2	08HYI2	08HYI2 macropus eu
164	255	28.1	186	1	INB3_BOVIN	P01577 bos taurus	237	94.5	10.4	84	2	Q95LH8	Q95LH8 sus scrofa
165	254.5	28.1	170	2	Q291I5	Q291I5 sus scrofa	238	90.5	10.0	84	2	Q95LH8	Q95LH8 sus scrofa
166	254	28.0	182	2	06XZW7	06XZW7 cachygiossu	239	90	9.9	1182	2	Q8IDJ0	Q8IDJ0 plasmodium
167	253.5	27.9	187	1	INB_HUMAN	P01574 homo sapien	240	89.5	9.9	68	2	08HYG4	08HYG4 macropus eu
168	253.5	27.9	187	2	Q776I2	Q776I2 macaca fasc	241	87.5	9.6	68	2	08HYI1	08HYI1 macropus eu
169	251	27.7	186	1	INB_FELCA	Q9N210 felis silve	242	85.5	9.4	2239	2	Q81BW8	Q81BW8 plasmodium
170	250.5	27.6	170	2	Q291I4	Q291I4 sus scrofa	243	85	9.4	253	2	Q66ZV9	Q66ZV9 borella ga
171	241.5	26.6	187	2	Q15943	Q15943 homo sapien	244	85	9.4	1920	1	PCTR_MOUSE	P48725 mus musculus
172	235.5	26.0	207	2	Q9P0W0	Q9P0W0 homo sapien	245	84.5	9.3	186	1	ATPF_MESVI	Q9MUT1 mesostigma
173	233	25.7	192	2	080ZFF2	080ZFF2 mus musculus	246	84	9.3	167	2	Q8EBD1	Q8EBD1 oceanobacill
174	230.5	25.4	186	1	INB1_BOVIN	P01578 bos taurus	247	83	9.2	241	2	Q9M1R0	Q9M1R0 arabidopsis
175	227	25.0	99	2	Q75T05	Q75T05 cyccolagus	248	83	9.2	2838	2	Q8VHU9	Q8VHU9 rattus norv
176	226.5	25.0	183	2	Q7YRX6	Q7YRX6 macropus eu	249	82.5	9.1	297	2	Q9H5C1	Q9H5C1 homo sapien
177	199.5	22.0	182	2	Q9R1T0	Q9R1T0 mus musculus	250	82	9.0	496	2	Q42434	Q42434 notophthalm

251	82	9.0	581	2	06Y5M8	06Y5M8 mus musculus	324	76.5	8.4	854	2	06NUP4	06NUP4 homo sapien
252	82	9.0	805	2	09NCNS	09NCNS euploetes ae	325	76.5	8.4	1131	2	08Y143	08Y143 anabaena sp
253	82	9.0	1512	2	08CDL2	08CDL2 mus musculus	326	76.5	8.4	1465	2	07TP27	07TP27 rattus norv
254	82	9.0	1911	2	08OU10	08OU10 mus musculus	327	76.5	8.4	1705	2	07REB8	07REB8 plasmidium
255	81.5	9.0	302	2	06X853	06X853 streptococc	328	76	8.4	129	2	095235	095235 plasmidium
256	81.5	9.0	373	2	08VX54	08VX54 solanum tub	329	76	8.4	133	2	0964R4	0964R4 plasmidium
257	81.5	9.0	382	2	06UEH5	06UEH5 aspergillus	330	76	8.4	459	2	07SYF7	07SYF7 acipenser b
258	81.5	9.0	412	2	050371	050371 methylophil	331	76	8.4	511	2	08W117	08W117 arabidopsis
259	81.5	9.0	739	2	09M9G4	09M9G4 arabidopsis	332	76	8.4	519	1	YB29-STAN	YB29-STAN staphylococ
260	81.5	9.0	752	2	08RVQ6	08RVQ6 arabidopsis	333	76	8.4	519	1	YB69-STAM	YB69-STAM staphylococ
261	81.5	9.0	751	2	09A4I6	09A4I6 arabidopsis	334	76	8.4	519	1	YC86-STAM	YC86-STAM staphylococ
262	81.5	9.0	845	2	06NVC9	06NVC9 brachydanio	335	76	8.4	519	2	06G9S7	06G9S7 staphylococ
263	81.5	9.0	8407	2	07RTM4	07RTM4 homo sapien	336	76	8.4	519	2	06GHE9	06GHE9 straphylococ
264	81	8.9	136	2	070G08	070G08 oncorhynch	337	76	8.4	573	2	06E1R4	06E1R4 geobacillus
265	81	8.9	180	2	06SR85	06SR85 carassius a	338	76	8.4	573	2	06E1R5	06E1R5 geobacillus
266	81	8.9	309	2	08W1K2	08W1K2 crataerostig	339	76	8.4	573	2	06E1R6	06E1R6 geobacillus
267	81	8.9	332	1	NDP2_VIBVY	NDP2_VIBVY vibrio vuln	340	76	8.4	573	2	06E1R7	06E1R7 geobacillus
268	81	8.9	564	2	06C4J5	06C4J5 variowia li	341	76	8.4	574	2	0803C5	0803C5 brachydanio
269	81	8.9	873	2	098949	098949 gallus gall	342	76	8.4	605	2	07SYN2	07SYN2 brachydanio
270	81	8.9	2178	2	08I643	08I643 plasmidium	343	76	8.4	634	2	09PUD1	09PUD1 chlamydia m
271	80.5	8.9	301	2	08D220	08D220 erwina car	344	76	8.4	826	2	08TL94	08TL94 methanosa
272	80.5	8.9	407	2	06LH49	06LH49 photobacter	345	76	8.4	880	2	08QFP9	08QFP9 xenopus lae
273	80.5	8.9	581	1	CN67_YEAST	CN67_YEAST saccharomyc	346	75.5	8.3	187	2	090196	090196 spodoptera
274	80	8.8	350	2	09JMM4	09JMM4 wolbachia s	347	75.5	8.3	208	1	RS4_HAEDU	RS4_HAEDU drosophila
275	80	8.8	734	2	07OEG6	07OEG6 anopheles g	348	75.5	8.3	227	2	08M1C4	08M1C4 drosophila
276	80	8.8	2042	2	025766	025766 plasmidium	349	75.5	8.3	392	2	06H8K4	06H8K4 porcine par
277	79.5	8.8	344	2	097WC3	097WC3 sulfobolus	350	75.5	8.3	545	2	06DB26	06DB26 erwina car
278	79.5	8.8	378	1	TGT_VIBVU	TGT_VIBVU vibrio vuln	351	75.5	8.3	890	2	09DSP8	09DSP8 saint croix
279	79.5	8.8	433	2	TGT_VIBCH	TGT_VIBCH vibrio chol	352	75.5	8.3	1499	2	07QPE8	07QPE8 giardia lam
280	79.5	8.8	433	2	07MNH1	07MNH1 vibrio vuln	353	75	8.3	158	2	07NSM2	07NSM2 chromobacte
281	79.5	8.8	804	2	06FYE7	06FYE7 bartonella	354	75	8.3	160	2	07S7E0	07S7E0 neurospora
282	79.5	8.8	927	2	06CIS9	06CIS9 kluyveromyc	355	75	8.3	164	2	087124	087124 neurospora
283	79.5	8.8	2710	2	09XZB8	09XZB8 plasmidium	356	75	8.3	196	2	06LYV9	06LYV9 methanococ
284	79.5	8.8	3026	2	026030	026030 plasmidium	357	75	8.3	461	1	TRME_HELPU	TRME_HELPU helicobacte
285	79	8.7	897	2	06CGI4	06CGI4 variowia li	359	75	8.3	507	2	07ZXU4	07ZXU4 xenopus lae
286	78	8.6	290	2	06LL14	06LL14 photobacter	360	75	8.3	514	2	MR11_MOUSE	MR11_MOUSE mus muscu
287	78	8.6	331	1	RFOA_MOLSU	RFOA_MOLSU wolfinella s	361	75	8.3	573	2	06E1N0	06E1N0 geino bacillus sp
288	78	8.6	453	2	08BWD3	08BWD3 m mus muscu	362	75	8.3	573	2	06E1N2	06E1N2 geino bacillus th
289	78	8.6	487	2	061373	061373 drosophila	363	75	8.3	573	2	06E1N3	06E1N3 geino bacillus th
290	78	8.6	487	2	09VJ06	09VJ06 drosophila	364	75	8.3	573	2	06E1N4	06E1N4 geino bacillus st
291	78	8.6	488	1	K2C8_MOUSE	K2C8_MOUSE mus muscu	365	75	8.3	573	2	06E1N8	06E1N8 geino bacillus th
292	78	8.6	502	1	DCE1_ARATH	DCE1_ARATH arabidopsis	366	75	8.3	1503	1	06E1N9	06E1N9 geino bacillus th
293	78	8.6	680	2	08B1F3	08B1F3 m mus muscu	367	75	8.3	1821	2	MUKB_HAEDU	MUKB_HAEDU hamophilus
294	78	8.6	762	2	08BM85	08BM85 m mus muscu	368	75	8.3	213	1	07X8X4	07X8X4 oryza sativ
295	78	8.6	772	2	092555	092555 homo sapien	369	74.5	8.2	332	2	THAI_HUMAN	THAI_HUMAN homo sapien
296	78	8.6	1141	2	091Y79	091Y79 rattus norv	370	74.5	8.2	374	1	TGT_YERPE	TGT_YERPE mus muscu
297	78	8.6	1299	2	06GLR7	06GLR7 xenopus lae	371	74.5	8.2	374	1	066D95	066D95 pseudomonas
298	78	8.6	3255	2	09PKM8	09PKM8 chlamydia m	372	74.5	8.2	378	2	0898G5	0898G5 clostridium
299	78	8.6	496	1	WDJ7_MOUSE	WDJ7_MOUSE mus muscu	373	74.5	8.2	510	2	06C8T5	06C8T5 variowia li
300	77.5	8.5	1029	2	059809	059809 schizosacch	374	74.5	8.2	520	2	06DE01	06DE01 xenopus lae
301	77.5	8.5	1495	2	06CS07	06CS07 kluyveromyc	375	74.5	8.2	545	2	091B62	091B62 xenopus lae
302	77.5	8.5	1514	2	06B8R6	06B8R6 legionella	376	74.5	8.2	545	2	09HVN7	09HVN7 pseudomonas
303	77.5	8.5	247	2	081ZES	081ZES bacillus an	377	74.5	8.2	569	2	06P3G2	06P3G2 brachydanio
304	77.5	8.5	247	2	06HP78	06HP78 bacillus th	378	74.5	8.2	657	2	07UZL3	07UZL3 proclostridio
305	77	8.5	562	2	09Z3J1	09Z3J1 mus muscu	379	74.5	8.2	758	1	GOA1_MOUSE	GOA1_MOUSE mus muscu
306	77	8.5	573	2	06E1N7	06E1N7 bacillus th	380	74.5	8.2	897	2	08ASR6	08ASR6 bacteroides
307	77	8.5	576	1	REC_N_BACSU	REC_N_BACSU bacillus su	381	74.5	8.2	1092	2	06L3H7	06L3H7 solanum dem
308	77	8.5	879	2	096GV6	096GV6 homo sapien	382	74.5	8.2	1162	2	0754X1	0754X1 aabhyra goss
309	77	8.5	893	2	08KKY1	08KKY1 rhizobium e	383	74.5	8.2	1906	2	0813H0	0813H0 plasmidium
310	77	8.5	893	2	08TEA7	08TEA7 homo sapien	384	74.5	8.2	8797	1	SNE1_HUMAN	SNE1_HUMAN homo sapien
311	77	8.5	115	2	059193	059193 pyrococcus	385	74.5	8.2	127	2	08QOQ7	08QOQ7 equid herpe
312	76.5	8.4	191	2	09H7K0	09H7K0 homo sapien	386	74.5	8.2	220	2	064QR4	064QR4 bacteroides
313	76.5	8.4	213	2	06IA39	06IA39 homo sapien	387	74	8.2	243	2	06YJ03	06YJ03 onion yello
314	76.5	8.4	230	2	06E9F2	06E9F2 acinetobact	388	74	8.2	295	2	07NIG2	07NIG2 gloeobacter
315	76.5	8.4	287	2	08R2V2	08R2V2 mus muscu	389	74	8.2	382	2	07VLD4	07VLD4 haemophilus
316	76.5	8.4	322	2	06B0C0	06B0C0 debaromyce	390	74	8.2	533	2	06S101	06S101 uncultured
317	76.5	8.4	375	2	06LU69	06LU69 photobacter	391	74	8.2	874	2	09Y166	09Y166 brachydanio
318	76.5	8.4	375	2	06LU69	06LU69 photobacter	392	74	8.2	1431	2	09NG75	09NG75 paratemia
319	76.5	8.4	375	2	06LU69	06LU69 photobacter	393	74	8.2				
320	76.5	8.4	375	2	06LU69	06LU69 photobacter	394	74	8.2				
321	76.5	8.4	375	2	06LU69	06LU69 photobacter	395	74	8.2				
322	76.5	8.4	375	2	06LU69	06LU69 photobacter	396	74	8.2				
323	76.5	8.4	375	2	06LU69	06LU69 photobacter	396	74	8.2				

397	74	8.2	1802	2	048647	048647 oryza sativ	470	72	7.9	397	2	07PW81	07PW81 anopheles g		
398	74	8.2	4041	2	06FMG2	06fmg2 candida gla	471	72	7.9	467	2	09GCV0	09GCV0 triatolepi		
399	73.5	8.1	269	2	094238	094238 caenorhabdi	472	72	7.9	487	2	061518	061518 mus musculu		
400	73.5	8.1	312	2	08BVN7	08BVN7 mus musculu	473	72	7.9	490	2	061463	061463 mus musculu		
401	73.5	8.1	367	2	061PP6	061pp6 homo sapien	474	72	7.9	509	2	08HUG6	08HUG6 seebania ve		
402	73.5	8.1	375	2	095PO5	095po5 molgula ocu	475	72	7.9	517	2	08T768	08T768 branchiostec		
403	73.5	8.1	435	1	SNXR_HUMAN	096192 homo sapien	476	72	7.9	598	2	09LUN4	09LUN4 arabadopsis		
404	73.5	8.1	446	2	08VX56	08VX56 solanum tub	477	72	7.9	601	2	06TLH1	06TLH1 brachydanio		
405	73.5	8.1	478	2	086632	086632 beet crypti	478	72	7.9	674	2	09XIS8	09XIS8 chlamydia p		
406	73.5	8.1	519	2	080T21	080T21 mus musculu	479	72	7.9	680	2	09Z7B0	09Z7B0 chlamydia p		
407	73.5	8.1	532	2	07TOL6	07TOL6 mus musculu	480	72	7.9	745	2	073K85	073K85 treponema d		
408	73.5	8.1	549	1	TBC3_HUMAN	081zpi homo sapien	481	72	7.9	758	2	044893	044893 caenorhabdi		
409	73.5	8.1	549	2	061PX1	061px1 homo sapien	482	72	7.9	796	2	049464	049464 arabadopsis		
410	73.5	8.1	704	2	09U2J3	09u2j3 caenorhabdi	483	72	7.9	868	2	098G31	098G31 rhizobium 1		
411	73.5	8.1	813	1	PEPX_LACPL	088y02 lactobacilli	484	72	7.9	1066	1	SVI_PYRPU	SVI_PYRPU		
412	73.5	8.1	817	2	09BUT1	09buj1 caenorhabdi	485	72	7.9	1471	2	07QF02	07QF02 giardia lam		
413	73.5	8.1	894	2	08EGS1	08egb1 shewanella	486	72	7.9	1851	2	09ESP3	09ESP3 rattus norv		
414	73.5	8.1	984	2	093HT8	093ht8 clostridium	487	72	7.9	2215	2	086D77	086D77 varroa deest		
415	73.5	8.1	1034	2	06LX78	06LX78 methanococc	488	72	7.9	4589	2	076506	076506 tetrahymena		
416	73.5	8.1	1149	2	09P8H7	09P8H7 candida alb	489	72	7.9	4924	2	09P7T1	09P7T1 echinosacch		
417	73.5	8.1	1956	2	09V2K3	09V2K3 homo sapien	490	72	7.9	168	2	075S22	075S22 brachydanio		
418	73	8.0	265	2	06MQS7	06mqst bdellovibri	491	72	7.9	179	2	0800H1	0800H1 brachydanio		
419	73	8.0	341	1	TAF7_MOUSE	091ic0 mus musculu	492	72	7.9	183	2	0800G9	0800G9 brachydanio		
420	73	8.0	360	2	07Q896	07Q896 anopheles g	493	72	7.9	185	2	08AY12	08AY12 brachydanio		
421	73	8.0	408	2	06C0L6	06C0L6 Yarrowia li	494	72	7.9	217	2	09VYR0	09VYR0 dtrosophila		
422	73	8.0	472	2	06D3Q2	06d3q2 erwina car	495	72	7.9	269	2	06Z248	06Z248 oryza sativ		
423	73	8.0	484	2	09OY24	09OY24 mus musculu	496	72	7.9	353	2	09S832	09S832 arabadopsis		
424	73	8.0	493	2	015872	015872 paramecium	497	72	7.9	375	1	TGT_SALTY	TGT_SALTY		
425	73	8.0	493	2	08L9X0	08L9X0 arabadopsis	498	72	7.9	433	2	09V587	09V587 brachydanio		
426	73	8.0	517	2	06K5H5	06K5H5 oryza sativ	499	72	7.9	421	2	08T320	08T320 dtrosophila		
427	73	8.0	519	2	061G01	061g01 rattus norv	500	72	7.9	434	2	08BQK5	08BQK5 mus musculu		
428	73	8.0	534	2	09CAB0	09cab0 arabadopsis	501	72	7.9	494	2	08ENM2	08ENM2 oceanobacilli		
429	73	8.0	553	2	09Z3J3	09z3j3 mus musculu	502	72	7.9	522	2	09C9T9	09C9T9 arabadopsis		
430	73	8.0	622	2	Q7YU54	Q7YU54 dtrosophila	503	72	7.9	549	2	06DHY5	06DHY5 homo sapien		
431	73	8.0	622	2	Q9V3I3	Q9V3I3 dtrosophila	504	72	7.9	556	2	0836P9	0836P9 enterococcu		
432	73	8.0	659	1	UVRB_CLOPE	046323 clostridium	505	72	7.9	559	2	09DID9	09DID9 influenza a		
433	73	8.0	742	2	Q95JY6	Q95jy6 macaca fasc	506	72	7.9	607	2	09Y8U6	09Y8U6 aeropyrum p		
434	73	8.0	855	2	08CDK1	08cdk1 mus musculu	507	72	7.9	633	2	P73606	P73606 synechocyst		
435	73	8.0	947	1	RGAS3_SOJBU	07xao0 solanum bul	508	72	7.9	651	1	UVRB_BACSU	UVRB_BACSU		
436	73	8.0	1085	1	CUTT7_SCHPO	P24339 echinosacch	509	72	7.9	71.5	7.9	661	1	YNRH_CAEEL	YNRH_CAEEL
437	73	8.0	1972	1	MYHB_MOUSE	008638 mus musculu	510	72	7.9	820	1	Q6Z5S4	Q6Z5S4 caenorhabdi		
438	73	8.0	1972	2	08R384	08R384 mus musculu	511	72	7.9	830	1	GYRA_CLOAB	GYRA_CLOAB		
439	73	8.0	1984	2	0692X3	0692x3 mus musculu	512	72	7.9	856	2	062121	062121 mus musculu		
440	72.5	8.0	166	1	RUVX_RHILLO	098m90 rhizobium 1	513	72	7.9	887	1	UFO_HUMAN	UFO_HUMAN		
441	72.5	8.0	208	2	0749B2	0749B2 geobacter s	514	72	7.9	948	2	08A3E9	08A3E9 bacteroides		
442	72.5	8.0	212	2	Q8ND60	Q8nd60 homo sapien	515	72	7.9	1052	2	07Z7R0	07Z7R0 homo sapien		
443	72.5	8.0	324	2	Q7R3C9	Q7R3C9 giardia lam	516	72	7.9	1204	2	094HV3	094HV3 oryza sativ		
444	72.5	8.0	368	2	06BGA0	06bgao paramecium	517	72	7.9	1204	2	07XRF26	07XRF26 oryza sativ		
445	72.5	8.0	374	2	Q7MB01	Q7mb01 photorhabdu	518	72	7.9	1290	1	RA50_SCHPO	RA50_SCHPO		
446	72.5	8.0	456	2	06BHQ4	06bhq4 debaryomyce	519	72	7.9	1489	2	06B145	06B145 debaryomyce		
447	72.5	8.0	556	2	07R198	07r198 plasmodium	520	72	7.9	1501	2	06B146	06B146 debaryomyce		
448	72.5	8.0	558	2	07MB08	07mbg8 vibrio vuln	521	72	7.9	1972	1	MYHB_HUMAN	MYHB_HUMAN		
449	72.5	8.0	568	2	08D4X9	08d4x9 vibrio vuln	522	72	7.9	2023	2	09V5Z9	09V5Z9 dtrosophila		
450	72.5	8.0	661	2	0659H3	0659h3 bacillus am	523	72	7.9	2035	1	NIN_MOUSE	NIN_MOUSE		
451	72.5	8.0	720	2	08N7X3	08n7x3 homo sapien	524	72	7.9	2113	2	0674R4	0674R4 mus musculu		
452	72.5	8.0	721	1	BBS2_HUMAN	09bxc9 homo sapien	525	72	7.9	2136	2	0674R4	0674R4 mus musculu		
453	72.5	8.0	735	2	Q7VSE4	07VSE4 prochloroco	526	72	7.9	2136	2	0674R4	0674R4 mus musculu		
454	72.5	8.0	822	1	WJCE_YEAST	P47061 seccaromyce	527	72	7.9	2136	2	0674R4	0674R4 mus musculu		
455	72.5	8.0	892	1	SYA_HELHP	Q7VHV4 helicobacte	528	72	7.9	3200	2	07XEP7	07XEP7 oryza sativ		
456	72.5	8.0	980	2	024780	024780 clostridium	529	72	7.9	5633	2	081454	081454 plasmodium		
457	72.5	8.0	1053	2	06BG20	06bg20 paramecium	530	72	7.8	226	1	DP1A_ECOLI	DP1A_ECOLI		
458	72.5	8.0	1289	2	068DM1	068dm1 homo sapien	531	72	7.8	288	1	PSTB_MYCPE	PSTB_MYCPE		
459	72.5	8.0	1585	2	07Z745	07z745 homo sapien	532	72	7.8	310	2	028810	028810 potocorus tr		
460	72.5	8.0	2241	2	08IKJ7	08ikj7 plasmodium	533	72	7.8	316	2	0735I6	0735I6 bacillus ce		
461	72.5	8.0	2411	2	06CXV6	06cxv6 kluuyetomye	534	72	7.8	316	2	081BM4	081bm4 bacillus ce		
462	72.5	8.0	3911	1	ACA9_HUMAN	099996 h a-kinase	535	72	7.8	353	2	09JMP1	09JMP1 bacterioph		
463	72	7.9	127	2	06B598	06B598 asinine her	536	72	7.8	372	2	09P3F1	09P3F1 neurospora		
464	72	7.9	210	2	064848	064848 porcine ade	537	72	7.8	378	1	MAT1_COCSA	09P446 cochlilobu		
465	72	7.9	247	2	07YV22	07YV22 cryptospori	538	72	7.8	389	2	07SA30	07sa30 neurospora		
466	72	7.9	297	2	06SF19	06sf19 uncultured	539	72	7.8	415	2	09LRW6	09LRW6 arabadopsis		
467	72	7.9	319	2	06D077	06d077 erwina car	540	72	7.8	474	2	096W63	096W63 homo sapien		
468	72	7.9	341	2	06R1L1	06r1l1 cricetus	541	72	7.8	503	1	CPV1_LAGAC	CPV1_LAGAC		
469	72	7.9	381	2	08FSM7	08fsm7 corynebacte	542	72	7.8	505	1	RADA_SYNY3	P74391 synechocyst		

543	71	7.8	552	2	Q6NSC0	Q6nsco homo sapien	616	70	7.7	431	2	Q6SXY7	Q6sxy7 drosophila
544	71	7.8	634	2	Q6P3C2	Q6p3c2 xanthomonas	617	70	7.7	438	2	Q6MVZ4	Q6mvz4 leucodon ac
545	71	7.8	641	2	Q7RXA7	Q7rxax7 neurospora	618	70	7.7	448	1	RUI7_DROME	P17133 drosophila
546	71	7.8	713	2	Q7NSZ9	Q7nsz9 photorhabdu	619	70	7.7	448	2	Q974Y6	Q974y6 sulfolobus
547	71	7.8	716	1	HOKJ2_MOUSE	Q7mk6 mus musculu	620	70	7.7	449	2	Q9CS90	Q9cs90 arabidopsis
548	71	7.8	716	2	Q6GJV2	Q6gfv2 mus musculu	621	70	7.7	463	2	Q8BP23	Q8bp23 xanthomonas
549	71	7.8	722	2	Q8YRW1	Q8yrw1 anabaena sp	622	70	7.7	493	2	P957J2	P957j2 salmonella
550	71	7.8	757	1	PEPX_STRPN	Q9rxc8 streptococc	623	70	7.7	508	2	Q6NVR6	Q6nvr6 xenopus tro
551	71	7.8	757	1	PEPX_STRK6	Q8q87 streptococc	624	70	7.7	513	2	Q9LRU0	Q9lru0 triticum ae
552	71	7.8	806	1	NH48_CAEEL	Q9407 caenorhabdi	625	70	7.7	541	2	Q7SS55	Q7ss55 neurospora
553	71	7.8	806	1	SYL_HELPJ	Q9z163 helicobacte	626	70	7.7	573	2	Q6EIP0	Q6eip0 bacillus sp
554	71	7.8	857	2	Q7PDB6	Q7pdb6 anopheles g	627	70	7.7	584	2	Q97H15	Q97h15 clostridium
555	71	7.8	1029	2	Q63BK4	Q63bk4 bacillus ce	628	70	7.7	587	2	Q9RA89	Q9ra89 sinorhizobi
556	71	7.8	1029	2	Q81Q09	Q81qg9 bacillus an	629	70	7.7	600	2	Q15516	Q15516 homo sapien
557	71	7.8	1029	2	Q6HJ13	Q6hj13 bacillus th	630	70	7.7	663	2	Q756H5	Q756h5 ashbya goss
558	71	7.8	1271	2	Q8A321	Q8a321 bacteroides	631	70	7.7	675	2	Q8ZJ52	Q8zj52 streptomyce
559	71	7.8	1742	2	Q81U0U	Q81u0u plasmodium	632	70	7.7	686	2	Q71RW7	Q71rw7 pantoea agg
560	71	7.8	1749	2	Q81IM5	Q81im5 plasmodium	633	70	7.7	714	2	Q15718	Q15718 dictyosteli
561	71	7.8	1761	2	Q81O91	Q81o91 plasmodium	634	70	7.7	742	2	Q7X4V0	Q7x4v0 bacillus ce
562	71	7.8	2819	2	Q98QF8	Q98qf8 mycoplasma	635	70	7.7	742	2	Q7X4V1	Q7x4v1 bacillus an
563	70.5	7.8	153	2	Q8C8P3	Q8c8p3 m mus muscu	636	70	7.7	792	2	Q9BP03	Q9bp03 dictyosteli
564	70.5	7.8	185	2	Q8O0H0	Q8o0h0 brachydanio	637	70	7.7	795	2	Q751F8	Q751f8 ashbya goss
565	70.5	7.8	196	2	Q76KAS	Q76kas brachydanio	638	70	7.7	823	2	Q73FK0	Q73fk0 bacillus ce
566	70.5	7.8	231	2	Q6CPN5	Q6cpn5 kluyveromyc	639	70	7.7	823	2	Q81WQ3	Q81wq3 bacillus an
567	70.5	7.8	248	2	P90930	P90930 caenorhabdi	640	70	7.7	823	2	Q6H009	Q6h009 bacillus th
568	70.5	7.8	253	1	PSTB_CLOPE	Q8xmp8 clostridium	641	70	7.7	890	2	Q45S87	Q45s87 caenorhabdi
569	70.5	7.8	265	2	Q639N3	Q639n3 bacillus ce	642	70	7.7	939	2	Q7Q3F0	Q7q3f0 anopheles g
570	70.5	7.8	265	2	Q923V9	Q923v9 pseudomonas	643	70	7.7	1067	1	SVI_PYRAB	Q9v072 pyrococcus
571	70.5	7.8	316	1	GSBH_PHOLL	Q7m7h8 photorhabdu	644	70	7.7	1157	2	Q6NP14	Q6np14 drosophila
572	70.5	7.8	349	2	Q7VIT4	Q7vit4 helicobacte	645	70	7.7	1310	2	Q861X0	Q861x0 dictyosteli
573	70.5	7.8	357	2	Q9S320	Q9s320 homo sapien	646	70	7.7	2871	1	DESP_HUMAN	P15924 homo sapien
574	70.5	7.8	381	2	Q6D855	Q6d855 erwina car	647	70	7.7	3218	2	Q9W3T6	Q9w3t6 drosophila
575	70.5	7.8	415	2	Q9SJW7	Q9sjw7 arabidopsis	648	70	7.7	120	2	Q9NHM1	Q9nhm1 plasmodium
576	70.5	7.8	425	2	Q6AYE4	Q6aye4 raltus norv	649	69.5	7.7	224	2	Q678L1	Q678l1 mus musculu
577	70.5	7.8	513	2	Q6CRJ1	Q6cjr1 kluyveromyc	650	69.5	7.7	285	2	Q9L3N0	Q9l3n0 microcycis
578	70.5	7.8	519	1	Y964_STARP	Q8scs7 strephilococ	651	69.5	7.7	415	2	Q50861	Q50861 mycobacteri
579	70.5	7.8	558	2	Q8N7M4	Q8n7m4 homo sapien	652	69.5	7.7	415	2	Q70J57	Q70j57 microcycis
580	70.5	7.8	558	2	Q9X225	Q9x225 thermotoga	653	69.5	7.7	417	2	Q6D4N9	Q6d4n9 erwina car
581	70.5	7.8	656	1	YC26_PORPU	P51392 porphyra pu	654	69.5	7.7	427	2	Q99160	Q99160 mus musculu
582	70.5	7.8	660	1	LYRB_BACHD	Q9k6x9 bacillus ha	655	69.5	7.7	437	2	Q6PHA4	Q6pha4 mus musculu
583	70.5	7.8	719	1	HOKJ2_HUMAN	Q9ed9 homo sapien	656	69.5	7.7	452	2	P73256	P73256 synechocyst
584	70.5	7.8	733	2	Q6GJF2	Q6gfj2 mus musculu	657	69.5	7.7	457	1	BAG4_HUMAN	Q95429 homo sapien
585	70.5	7.8	839	2	Q97FP9	Q97fp9 clostridium	658	69.5	7.7	476	2	Q647Q8	Q647q8 uncultured
586	70.5	7.8	863	1	MSP_ECHGR	P33417 echinococcu	659	69.5	7.7	505	2	Q6B1Z9	Q6biz9 debaromyce
587	70.5	7.8	863	1	MYSF_TAESA	Q8i305 taenia sagi	660	69.5	7.7	526	2	Q8K4T6	Q8k4t6 raltus norv
588	70.5	7.8	863	1	MYSF_TAESO	P33418 taenia sagi	661	69.5	7.7	541	2	Q941J3	Q941j3 zea mays (m
589	70.5	7.8	863	2	Q68JF3	Q68jf3 taenia soli	662	69.5	7.7	572	2	Q61FZ6	Q61fz6 mus musculu
590	70.5	7.8	892	1	RA16_SCHPO	P36617 schizosacch	663	69.5	7.7	594	2	Q73927	Q73927 squalus aca
591	70.5	7.8	1029	2	P91176	P91176 caenorhabdi	664	69.5	7.7	610	2	Q66FY3	Q66fy3 yersinia ps
592	70.5	7.8	1039	2	Q23461	Q23461 arabidopsis	665	69.5	7.7	610	2	Q8ZAG8	Q8zag8 yersinia ps
593	70.5	7.8	1137	2	Q8B159	Q8b159 mus musculu	666	69.5	7.7	623	2	Q72QY7	Q72qy7 leptospira
594	70.5	7.8	1192	2	Q8B179	Q8b179 mus musculu	667	69.5	7.7	623	2	Q8F4V3	Q8f4v3 leptospira
595	70.5	7.8	1235	2	Q8SK64	Q8sk64 drosophila	668	69.5	7.7	625	2	Q6IMF3	Q6imf3 raltus norv
596	70.5	7.8	1254	2	Q81ZW9	Q81zw9 homo sapien	669	69.5	7.7	661	2	Q65ED8	Q65ed8 bacillus li
597	70.5	7.8	1264	2	Q8GUS6	Q8gus6 oryza sativ	670	69.5	7.7	662	2	Q80MS5	Q80ms5 mus musculu
598	70.5	7.8	1286	2	Q6EUW7	Q6euw7 homo sapien	671	69.5	7.7	669	2	Q8BT4	Q8bt4 m mus muscu
599	70.5	7.8	1329	2	Q6FT10	Q6ft10 candida gla	672	69.5	7.7	675	2	Q8BMT4	Q8bmt4 m mus muscu
600	70.5	7.8	1381	2	Q9VZT7	Q9vzt7 drosophila	673	69.5	7.7	721	2	Q8BU17	Q8bu17 mus musculu
601	70.5	7.8	1450	2	Q8S119	Q8s119 oryza sativ	674	69.5	7.7	746	2	Q7VPE6	Q7vpe6 haemophilus
602	70.5	7.8	1515	2	Q6AVS6	Q6avs6 oryza sativ	675	69.5	7.7	788	2	Q8SVG1	Q8svg1 drosophila
603	70.5	7.8	1759	2	Q72PFO	Q72pfo leptospira	676	69.5	7.7	788	2	Q9W4N2	Q9w4n2 drosophila
604	70.5	7.8	1759	2	Q8F6Y5	Q8f6y5 leptospira	677	69.5	7.7	822	2	Q6B831	Q6b831 yersinia ps
605	70.5	7.8	2270	2	Q9KBA2	Q9kba2 plasmodium	678	69.5	7.7	832	2	Q6FNV5	Q6fnv5 yersinia ps
606	70.5	7.8	179	2	Q9KBA2	Q9kba2 bacillus ha	679	69.5	7.7	833	2	Q6FNV5	Q6fnv5 candida gla
607	70.5	7.8	209	2	Q8A8G4	Q8a8g4 bacteroides	680	69.5	7.7	843	2	Q74UL6	Q74ul6 yersinia pe
608	70.5	7.7	249	2	Q7MOS9	Q7mos9 wolinnella s	681	69.5	7.7	843	2	Q8D0D4	Q8d0d4 yersinia pe
609	70.5	7.7	316	2	Q639G4	Q639g4 bacillus ce	682	69.5	7.7	860	2	Q9FHN0	Q9fhn0 arabidopsis
610	70.5	7.7	326	2	Q7NMU0	Q7njd0 gloeobacter	683	69.5	7.7	866	2	Q25517	Q25517 helicobacte
611	70.5	7.7	326	2	Q6HMO1	Q6hmq1 bacillus th	684	69.5	7.7	894	2	Q8NSL2	Q8nsl2 homo sapien
612	70.5	7.7	332	2	Q8YND8	Q8ynd8 anabaena sp	685	69.5	7.7	912	2	Q6CEZ7	Q6cez7 yarrowia li
613	70.5	7.7	357	2	Q63168	Q63168 burkholderi	686	69.5	7.7	1041	2	Q7KWK7	Q7kwk7 dictyosteli
614	70.5	7.7	385	2	Q64V44	Q64v44 bacteroides	687	69.5	7.7	1139	1	LIPA_CAEEL	Q21049 caenorhabdi
615	70.5	7.7	399	2	Q9VZE1	Q9vze1 pyrococcus	688	69.5	7.7	1313	2	Q8X0S9	Q8x0s9 neurospora

689	69.5	7.7	1508	2	Q6BVU5	Q6bvus debaryomyce	762	68.5	7.6	207	2	Q6SGZ5	Q6sgz5 uncultured
690	69.5	7.7	1707	2	Q8YU12	Q8yu12 arabidops	763	68.5	7.6	207	2	Q6UCR9	Q6ucr9 uncultured
691	69.5	7.7	2052	2	Q7XW15	Q7xw15 oryza sativ	764	68.5	7.6	208	2	Q72CF5	Q72cf5 desulfovibr
692	69.5	7.7	2223	2	Q8IDJ2	Q8idj2 plasmodium	765	68.5	7.6	209	1	RS4_THEMEA	Q2x13 thermotoga
693	69	7.6	114	2	Q9MCW2	Q9mcw2 bacterioph	766	68.5	7.6	220	2	Q6UKI7	Q6uki7 capsicum an
694	69	7.6	116	2	Q64HN7	Q64hn7 bacterioph	767	68.5	7.6	240	2	Q65GA9	Q65ga9 bacillus ii
695	69	7.6	164	2	Q53357	Q53357 lactococcus	768	68.5	7.6	252	2	Q9BLO5	Q9bli5 leishmania
696	69	7.6	205	2	Q83VA7	Q83va7 western x p	769	68.5	7.6	294	2	Q6AVJ9	Q6avj9 desulfotale
697	69	7.6	206	1	RS4_BUCAP	P41186 buchiera ap	770	68.5	7.6	295	2	Q8XNT6	Q8xnt6 streptylcoc
698	69	7.6	220	1	KAD_PYRRU	Q8u207 pyrococcus	771	68.5	7.6	295	2	Q6GBJ9	Q6gbj9 streptylcoc
699	69	7.6	231	2	Q7Q6E1	Q7q6e1 anopheles g	772	68.5	7.6	301	2	Q8ITG8	Q8itg8 methanosaer
700	69	7.6	247	2	Q63GQ6	Q63gq6 bacillus ce	773	68.5	7.6	304	2	Q7RCL1	Q7rc1 plasmodium
701	69	7.6	265	2	Q7MQP3	Q7mqf3 vibrio vuln	774	68.5	7.6	304	2	Q7RLJ4	Q7rlj4 plasmodium
702	69	7.6	265	2	Q8DDA9	Q8dda9 vibrio vuln	775	68.5	7.6	332	2	Q9Z6Z5	Q9z6z5 sulfolobus
703	69	7.6	272	1	HAT5_ABATH	Q00283 arabidopsis	776	68.5	7.6	363	2	Q6YXP5	Q6yxp5 onion yello
704	69	7.6	290	2	Q6N757	Q6n757 rhodospheudo	777	68.5	7.6	364	2	Q83SD5	Q83sd5 shigella fl
705	69	7.6	312	2	Q823T9	Q823t9 chlamydophi	778	68.5	7.6	367	1	MTCL_CHV13	P36218 chlorella v
706	69	7.6	321	2	Q6D2B4	Q6d2b4 erwina car	779	68.5	7.6	392	1	RRPP_SVS	P11208 simian viru
707	69	7.6	346	1	LYSK_SUNSO	Q980W5 sulfolobus	780	68.5	7.6	392	2	Q6H8K8	Q6h8k8 simian para
708	69	7.6	349	1	TAFF_HUMAN	Q15545 homo sapien	781	68.5	7.6	398	2	Q7OIA8	Q7oia8 anopheles g
709	69	7.6	365	2	Q8DRV3	Q8drv3 streptococc	782	68.5	7.6	414	2	Q8R6T9	Q8r6t9 thermocamer
710	69	7.6	415	2	Q6ETC9	Q6etc9 oryza sativ	783	68.5	7.6	417	2	Q6VTU0	Q6vtu0 vibrio para
711	69	7.6	421	1	RFL_METUA	Q582J9 methanococc	784	68.5	7.6	431	1	SGK1_HUMAN	Q00141 homo sapien
712	69	7.6	438	2	Q9WVX2	Q9wvx2 myiabea fru	785	68.5	7.6	431	1	SGK1_MOUSE	Q9wv6 mus musculu
713	69	7.6	482	1	K2C8_HUMAN	P05787 homo sapien	786	68.5	7.6	431	2	Q68G05	Q68g05 rattus norv
714	69	7.6	482	1	K2C8_RAT	Q10758 rattus norv	787	68.5	7.6	442	1	TRME_MYCPN	P5104 mycoplasma
715	69	7.6	483	2	Q6GMT0	Q6gmt0 homo sapien	788	68.5	7.6	456	2	Q8K8A3	Q8k8a3 streptococc
716	69	7.6	483	2	Q8OWH8	Q8owh8 rattus sp.	789	68.5	7.6	468	2	Q8IR66	Q8ir66 bacillus an
717	69	7.6	486	2	Q91WT0	Q91wt0 mus musculu	790	68.5	7.6	481	2	Q7XNT0	Q7xnt0 oryza sativ
718	69	7.6	496	2	Q8ENB3	Q8enb3 oceanobacil	791	68.5	7.6	487	2	Q23501	Q23501 arabidopsis
719	69	7.6	501	2	Q659X5	Q659x5 escherichia	792	68.5	7.6	494	2	Q7TH54	Q7th54 influenza a
720	69	7.6	504	2	Q8PSS5	Q8fps5 corynebacte	793	68.5	7.6	497	2	Q85YR0	Q85yr0 euphorbia s
721	69	7.6	505	2	Q6P4C7	Q6p4c7 homo sapien	794	68.5	7.6	502	2	Q8MTC9	Q8mtc9 helicobis z
722	69	7.6	505	2	Q8RV51	Q8rv51 oryza sativ	795	68.5	7.6	504	1	SIK1_YEAST	Q12460 saccharomyc
723	69	7.6	505	2	Q7X7I6	Q7x7i6 oryza sativ	796	68.5	7.6	519	2	Q6NS85	Q6ns85 mus musculu
724	69	7.6	509	2	Q9LRI9	Q9lri9 triticum ae	797	68.5	7.6	539	2	Q8K4V4	Q8k4v4 rattus norv
725	69	7.6	513	1	RMUC_VIBCH	Q9kvt9 vibrio chol	798	68.5	7.6	546	2	Q6YZN1	Q6yzn1 oryza sativ
726	69	7.6	533	1	Q94G13	Q94g13 physcomitre	799	68.5	7.6	552	2	Q8DVB0	Q8dvb0 streptococc
727	69	7.6	567	2	Q8HON7	Q8hon7 populus tri	800	68.5	7.6	583	2	Q74WJ2	Q74wj2 yersinia pe
728	69	7.6	576	2	Q659H4	Q659h4 bacillus am	801	68.5	7.6	590	2	Q66CF2	Q66cf2 yersinia ps
729	69	7.6	582	2	Q6W9J5	Q6w9j5 paramecium	802	68.5	7.6	590	2	Q8ZG79	Q8zgt9 citrus unsh
730	69	7.6	613	2	Q6PG44	Q6pg44 homo sapien	803	68.5	7.6	621	2	Q6BE26	Q6be26 yersinia pe
731	69	7.6	633	2	Q6B8K3	P21174 pseudomonas	804	68.5	7.6	694	2	Q91870	Q91870 xenopus lae
732	69	7.6	670	1	UVRB_PSEAE	Q756Y5 aabhya gose	805	68.5	7.6	694	2	Q7ZYN2	Q7zyn2 xenopus lae
733	69	7.6	691	2	Q756Y5	P73259 streptococyt	806	68.5	7.6	718	2	Q8SMD8	Q8smd8 encephalito
734	69	7.6	715	2	P73259	Q75330 homo sapien	807	68.5	7.6	741	1	PI03_MOUSE	Q9j0e1 mus musculu
735	69	7.6	724	1	HMNR_HUMAN	Q8cgt0 mus musculu	808	68.5	7.6	741	2	Q8LIAS	Q8lias rattus norv
736	69	7.6	732	2	Q8CGT0	Q8cgt6 eupletes oc	809	68.5	7.6	768	2	Q6LJR3	Q6ljr3 solanum dem
737	69	7.6	799	2	Q8MT65	Q8mt65 anopheles g	810	68.5	7.6	803	2	Q6FLS7	Q6fls7 candida gla
738	69	7.6	809	2	Q7PT27	Q7pt27 strongyloce	811	68.5	7.6	803	2	Q9P382	Q9p382 schizosacch
739	69	7.6	833	2	Q96442	Q96442 strongyloce	812	68.5	7.6	836	1	NOT3_YEAST	P6102 saccharomyc
740	69	7.6	860	2	Q93091	Q93091 human immun	813	68.5	7.6	836	2	Q6B2J3	Q6b2j3 saccharomyc
741	69	7.6	871	2	Q7TWT0	Q7tmt0 mus musculu	814	68.5	7.6	843	1	VAV_RAT	P54100 rattus norv
742	69	7.6	879	2	Q76978	Q76978 scypha raph	815	68.5	7.6	875	2	Q9ZKZ8	Q9zkt8 helicobacte
743	69	7.6	893	2	Q6DC15	Q6dc15 xenopus lae	816	68.5	7.6	879	2	Q8VI99	Q8vi99 rattus norv
744	69	7.6	978	2	Q66HN7	Q66hn7 dictyoscell	817	68.5	7.6	888	2	Q6PE80	Q6pe80 mus musculu
745	69	7.6	982	1	PPOL_SARPE	Q11208 sarcoptero	818	68.5	7.6	888	2	Q8VIA0	Q8via0 rattus norv
746	69	7.6	1081	2	Q9GNT2	Q9gnt2 paracentroc	819	68.5	7.6	888	2	Q8OYQ3	Q8oyq3 mus musculu
747	69	7.6	1081	2	Q9GOS8	Q9ggs8 strongyloce	820	68.5	7.6	920	2	Q9E176	Q9e176 rhodococcus
748	69	7.6	1153	2	Q92UC1	Q92uc1 rickettsia	821	68.5	7.6	935	1	IF38_MEDTR	Q9xhm1 medicago tr
749	69	7.6	1182	2	Q8CBA7	Q8cba7 mus musculu	822	68.5	7.6	937	2	Q9XGF5	Q9xgf5 solanum tub
750	69	7.6	1237	1	KEB1_RABIT	P18688 oryctolagus	823	68.5	7.6	938	2	Q9SM52	Q9sm52 solanum aca
751	69	7.6	1349	2	Q6RCM0	Q6rcm0 entamoeba h	824	68.5	7.6	948	2	Q9KPD4	Q9kpd4 vibrio chol
752	69	7.6	1437	2	Q8VDC1	Q8vdc1 mus musculu	825	68.5	7.6	988	2	Q7XIH2	Q7xih2 oryza sativ
753	69	7.6	1486	2	Q6LPL5	Q6lpl5 photobacter	826	68.5	7.6	1039	1	SYI_METUA	Q58357 methanococ
754	69	7.6	1633	2	Q88QC4	Q88qc4 pseudomonas	827	68.5	7.6	1108	2	Q63J03	Q63j03 bacillus ce
755	69	7.6	1860	2	Q6AVU8	Q6avu8 oryza sativ	828	68.5	7.6	1108	2	Q81KY5	Q81ky5 bacillus an
756	69	7.6	1898	2	Q6FNX9	Q6fnx9 candida gla	829	68.5	7.6	1108	2	Q6HCS8	Q6hcs8 bacillus th
757	69	7.6	1972	1	MYHB_RABIT	P35748 oryctolagus	830	68.5	7.6	1114	2	Q9NE53	Q9nes3 leishmania
758	69	7.6	2426	2	Q7PLZ8	Q7plz8 anopheles g	831	68.5	7.6	1132	1	DNBI_HHV6U	P52338 human herpe
759	68.5	7.6	153	2	Q9KRA3	Q9kra3 vibrio chol	832	68.5	7.6	1132	2	DNBI_HHV6Z	P52538 human herpe
760	68.5	7.6	206	2	RS4_CLOTE	Q8a0q9 clostridium	833	68.5	7.6	1132	2	Q785N4	Q785n4 human herpe
761	68.5	7.6	207	1	RS4_CANBF	Q7vqc4 candidatus	834	68.5	7.6	1162	1	SA2_MOUSE	Q15638 mus musculu

835	68.5	7.6	1162	2	06NZN7	06znt7 mus musculus	908	68	7.5	622	2	014794	014794 homo sapien
836	68.5	7.6	1242	1	KPB1_RAT	06k649 rattus norv	909	68	7.5	625	2	07NBZ6	07nbz6 mycoplasma
837	68.5	7.6	1270	2	06DKA2	06kka2 xenopus lae	910	68	7.5	639	2	0883E2	0883e2 pseudomonas
838	68.5	7.6	1292	2	06CF42	06cf42 yarrowia li	911	68	7.5	641	2	075CX7	075cx7 ashbya gos
839	68.5	7.6	1410	2	06NNX2	06nnx2 drosophila	912	68	7.5	696	2	08XQ93	08xq93 ralscopia s
840	68.5	7.6	1641	2	09VQ76	09vq76 drosophila	913	68	7.5	764	2	08LIL8	08lil8 oryza sativ
841	68.5	7.6	1960	2	08S6N2	08s6n2 oryza sativ	914	68	7.5	809	1	SYL_CAME	09pnk3 campylobact
842	68.5	7.6	2291	1	SPCB_DROME	000963 drosophila	915	68	7.5	842	1	CUL8_YEAST	07050 saccharomyc
843	68.5	7.6	2818	2	Q7SE15	Q7se15 neurospora	916	68	7.5	851	1	Q75OF1	Q75of1 ashbya gos
844	68	7.5	118	2	Q64HNS	Q64hns bacterioph	917	68	7.5	902	2	06BZAI	06bzai debrayomyce
845	68	7.5	244	2	Q9V0X5	Q9v0x5 pyrococcus	918	68	7.5	989	1	SUL1_DROME	08njg9 drosophila
846	68	7.5	247	1	PCPC_SPHCR	003520 sphinobium	919	68	7.5	908	2	0871J3	0871j3 vibrio algi
847	68	7.5	257	2	08FO19	08fo19 corynebacte	920	68	7.5	973	2	074698	074698 candida alb
848	68	7.5	259	2	Q7UKJ7	Q7ukj7 rhodospirill	921	68	7.5	981	2	080UK9	080uk9 mus musculu
849	68	7.5	263	2	Q76289	Q76289 helicoidari	922	68	7.5	994	1	MERK_MOUSE	060805 mus musculu
850	68	7.5	283	2	Q7MG66	Q7mgc6 vibrio vuln	923	68	7.5	1004	2	08UMH4	Q8umh4 human immun
851	68	7.5	297	2	06LJ73	Q6lj73 photobacter	924	68	7.5	1038	2	08VCU3	Q8vcu3 mus musculu
852	68	7.5	300	2	Q9X2S8	Q9x2s8 escherichia	925	68	7.5	1038	2	08CC88	Q8cc88 mus musculu
853	68	7.5	316	1	PGLB_CHICK	090944 gallus gall	926	68	7.5	1046	2	08J1Z6	08j1z6 iridovirus
854	68	7.5	326	1	SYRM_CHICK	P18561 rhizobium m	927	68	7.5	1063	2	093959	093959 candida alb
855	68	7.5	338	1	Q8UKC5	Q8ukc5 agrobacteri	928	68	7.5	1162	1	SA2_HUMAN	09h3u4 homo sapien
856	68	7.5	347	1	SH33_HUMAN	Q99963 homo sapien	929	68	7.5	1183	2	07T005	Q7t005 brachydanio
857	68	7.5	347	2	Q93RQ6	Q93rq6 streptococc	930	68	7.5	1231	2	06A102	Q6a102 homo sapien
858	68	7.5	361	2	Q7D3N9	Q7d3n9 agrobacteri	931	68	7.5	1231	2	06MZM4	Q6mzm4 homo sapien
859	68	7.5	365	2	Q8XJ95	Q8xj95 clostridium	932	68	7.5	1231	2	06MZM4	Q6mzm4 homo sapien
860	68	7.5	371	1	TCT_PSESM	Q867b0 pseudomonas	933	68	7.5	1268	2	068DE9	Q68de9 homo sapien
861	68	7.5	390	1	BIOP_HAETIN	P44422 haemophilus	934	68	7.5	1318	2	Q7QAJ3	Q7qaj3 anopheles g
862	68	7.5	391	2	Q8K5V9	Q8k5v9 streptococc	935	68	7.5	1333	2	06BK99	Q6bk99 dictyosteli
863	68	7.5	411	2	Q8CES2	Q8ces2 mus musculu	936	68	7.5	1355	2	06FXJ5	Q6fxj5 candida gla
864	68	7.5	434	2	Q6M3S7	Q6m3s7 brachytherci	937	68	7.5	1680	2	09P1Z9	Q9p1z9 homo sapien
865	68	7.5	440	1	SCRC_HUMAN	P47872 homo sapien	938	68	7.5	1708	2	068DP5	Q68dp5 homo sapien
866	68	7.5	440	2	Q8IV17	Q8iv17 homo sapien	939	68	7.5	2139	2	007569	Q07569 entamoeba h
867	68	7.5	441	2	Q9MVX1	Q9mvx1 thuidium re	940	68	7.5	2240	1	CD89_DROME	Q0veui drosophila
868	68	7.5	444	1	RBL_BOTST	P36477 botrytis ma	941	68	7.5	2357	2	Q9DGM6	Q9dgm6 brachydanio
869	68	7.5	450	2	Q79MP4	Q79mp4 seetreria ma	942	68	7.5	4524	2	0813J9	Q813j9 plasmodium
870	68	7.5	465	2	Q9GIF7	Q9gif7 brochelella	943	68	7.5	5255	1	BACA_BACLI	Q88006 b bacteriac
871	68	7.5	471	2	Q9FF75	Q9ff75 arabidopsis	944	68	7.5	5317	2	08TA74	Q8ta74 hemientroc
872	68	7.5	473	2	Q8DUJ7	Q8duj7 synechococc	945	67.5	7.4	109	2	Q9V0Z2	Q9v0z2 pyrococcus
873	68	7.5	475	2	Q8HW59	Q8hw59 trismegisti	946	67.5	7.4	135	2	P91417	P91417 caenorhadi
874	68	7.5	475	2	Q95G49	Q95g49 trismegisti	947	67.5	7.4	145	2	Q8JRV8	Q8jrv8 plithorimaea
875	68	7.5	475	2	Q9GIF8	Q9gif8 brochelella	948	67.5	7.4	170	2	064RJ5	Q64rj5 bacteroides
876	68	7.5	475	2	Q9TMS7	Q9tms7 heterophyll	949	67.5	7.4	211	2	06YQJ6	Q6yqj6 onion yello
877	68	7.5	475	2	Q9TMS5	Q9tms5 wijkia horn	950	67.5	7.4	215	2	Q86EV1	Q86ev1 schistosoma
878	68	7.5	475	2	Q9TMS6	Q9tms6 brochelella	951	67.5	7.4	251	2	P891J3	P891j3 sida golden
879	68	7.5	475	2	Q9TW73	Q9tmw3 boulaya mt	952	67.5	7.4	253	2	Q8WLD7	Q8wld7 acridocarpu
880	68	7.5	489	2	Q09051	Q09051 escherichia	953	67.5	7.4	254	2	Q8WLD7	Q8wld7 acridocarpu
881	68	7.5	490	2	Q9DBH4	Q9dbh4 mus musculu	954	67.5	7.4	267	2	Q8NDK7	Q8ndk7 tricomaria
882	68	7.5	493	2	Q8XB70	Q8xb70 escherichia	955	67.5	7.4	300	2	Q9SLI6	Q9slj6 arabidopsis
883	68	7.5	500	2	Q8FP06	Q8fp06 candida gla	956	67.5	7.4	302	2	Q6LPU3	Q6lpu3 photobacter
884	68	7.5	501	2	Q820Z7	Q820z7 shigella fl	957	67.5	7.4	319	2	Q8DHP4	Q8dhp4 synechococc
885	68	7.5	503	1	CPV1_CAPHI	Q6y121 capra hircu	958	67.5	7.4	326	2	Q71V08	Q71v08 homo sapien
886	68	7.5	503	1	CPV1_SHEEP	Q9x828 ovis aries	959	67.5	7.4	328	2	Q7W6Z8	Q7w6z8 bordetella
887	68	7.5	507	2	Q9SM61	Q9sm61 callithrix	960	67.5	7.4	360	2	Q659W3	Q659w3 homo sapien
888	68	7.5	507	2	Q8PA86	Q8pa86 escherichia	961	67.5	7.4	372	2	Q7Z3H1	Q7z3h1 homo sapien
889	68	7.5	511	2	Q90Z87	Q90z87 rana catesb	962	67.5	7.4	373	2	Q8FUF3	Q8fuf3 corynebacte
890	68	7.5	514	2	Q94IP9	Q94ip9 lycopersico	963	67.5	7.4	381	2	Q6A611	Q6a611 propionibac
891	68	7.5	537	2	Q93IEP9	Q93iep9 photorhabd	964	67.5	7.4	384	1	A1PL_HUMAN	Q9znz3 homo sapien
892	68	7.5	545	2	Q7QX89	Q7qx89 giardia lam	965	67.5	7.4	387	1	A1PL_PANPA	Q9smn3 pan panlicu
893	68	7.5	557	2	Q8A9T0	Q8a9t0 bacteroides	966	67.5	7.4	387	2	Q6CLZ4	Q6clz4 kluyveromyc
894	68	7.5	562	2	Q91V02	Q91v02 human immun	967	67.5	7.4	396	2	Q8BZY9	Q8bzy9 mus musculu
895	68	7.5	564	2	Q74Z82	Q74z82 ashbya gos	968	67.5	7.4	412	2	Q8SVZ5	Q8svz5 mus musculu
896	68	7.5	567	2	Q6J5H3	Q6j5h3 haemophilus	969	67.5	7.4	423	2	Q8ND86	Q8nd86 homo sapien
897	68	7.5	573	2	Q6E1P3	Q6e1p3 bacillus th	970	67.5	7.4	425	2	Q6FP05	Q6fp05 candida gla
898	68	7.5	573	2	Q6E1R9	Q6e1r9 bacillus th	971	67.5	7.4	427	2	Q8SVP6	Q8svp6 encephalito
899	68	7.5	573	2	Q6E1S1	Q6e1s1 bacillus sp	972	67.5	7.4	428	2	Q72LS2	Q72ls2 leptospira
900	68	7.5	573	2	Q6E1S2	Q6e1s2 geobacillus	973	67.5	7.4	428	2	Q8EY80	Q8ey80 leptospira
901	68	7.5	573	2	Q6E1S3	Q6e1s3 geobacillus	974	67.5	7.4	454	2	Q9SVG1	Q9svg1 arabidopsis
902	68	7.5	573	2	Q6E1S4	Q6e1s4 geobacillus	975	67.5	7.4	457	2	Q9SZM4	Q9szm4 arabidopsis
903	68	7.5	580	2	Q920F2	Q920f2 mus musculu	976	67.5	7.4	457	2	Q68A86	Q68a86 paratrichy
904	68	7.5	580	2	Q922U2	Q922u2 mus musculu	977	67.5	7.4	511	1	NIFK_SYN8	Q55030 synechococc
905	68	7.5	583	2	Q9ZQC5	Q9zqc5 arabidopsis	978	67.5	7.4	514	2	Q7PR88	Q7pr88 anopheles g
906	68	7.5	588	2	Q14729	Q14729 homo sapien	979	67.5	7.4	515	2	Q9CSW7	Q9csw7 arabidopsis
907	68	7.5	601	2	Q7SXW3	Q7sxw3 brachydanio	980	67.5	7.4	538	2	Q71AI2	Q71ai2 anaplasma m

981	67.5	7.4	539	2	06NXH9	06xrh9 mus musculus	1054	67	7.4	424	2	08T8M7	08t8m7 caenorhabdi
982	67.5	7.4	553	2	06IG03	06ig03 rattus norv	1055	67	7.4	429	2	094DF7	094df7 oryza sativ
983	67.5	7.4	555	2	09AV96	09av96 nicotiana t	1056	67	7.4	433	2	092TM4	092tm4 brachydanio
984	67.5	7.4	565	2	07OC70	07oc70 anopheles g	1057	67	7.4	435	2	09DMB4	09dmb4 rat cytoMeg
985	67.5	7.4	568	2	08OTC3	08otc3 mus musculu	1058	67	7.4	437	2	096379	096379 helianthus
986	67.5	7.4	583	2	08KMJ3	08kmj3 enterococcu	1059	67	7.4	438	2	08HT25	08ht25 isoplectryglo
987	67.5	7.4	615	2	06LIP9	06lip9 photobacter	1060	67	7.4	439	2	07V1A9	07v1a9 prochlorococ
988	67.5	7.4	636	2	06POF9	06pof9 anaplasma c	1061	67	7.4	446	2	0966M4	0966m4 caenorhabdi
989	67.5	7.4	657	2	06DD29	06dd29 xenopus lae	1062	67	7.4	446	2	070BL2	070bl2 mortierella
990	67.5	7.4	680	2	015740	015740 dictyosteli	1063	67	7.4	457	2	09UVV3	09uvv3 mortierella
991	67.5	7.4	719	2	09Y7B1	09y7b1 picchia past	1064	67	7.4	464	2	07VPF3	07vpf3 prochloroc
992	67.5	7.4	721	2	086M11	086m11 drosophila	1065	67	7.4	471	1	RFCL_HALNT1	rfcl_halnt1
993	67.5	7.4	722	2	09XC22	09xc22 mycoplasma	1066	67	7.4	475	2	094NB0	094nb0 gliosadelpH
994	67.5	7.4	723	2	06MSC5	06msc5 mycoplasma	1067	67	7.4	475	2	085V62	085v62 cratoneuron
995	67.5	7.4	758	2	06CPJ9	06cpj9 kluyveromyc	1068	67	7.4	475	2	09TMS9	09tms9 myuroclada
996	67.5	7.4	773	2	0806J1	0806j1 arabidopsis	1069	67	7.4	488	1	KL15_CAMEL	kl15_camel
997	67.5	7.4	803	2	06N012	06n012 homo sapien	1070	67	7.4	492	2	086LT6	086lt6 caenorhabdi
998	67.5	7.4	805	2	06F349	06f349 oryza sativ	1071	67	7.4	495	2	08RSV1	08rsv1 leptochrix
999	67.5	7.4	805	2	07MQJ4	07mqj4 vibrio vuln	1072	67	7.4	503	1	CPV1_BOVIN	cpv1_bovin
1000	67.5	7.4	805	2	08DDJ2	08ddj2 vibrio vuln	1073	67	7.4	509	2	09LBJ1	09lbj1 triticum ae
1001	67.5	7.4	837	2	06CKS5	06cks5 kluyveromyc	1074	67	7.4	535	2	065XU0	065xu0 oryza sativ
1002	67.5	7.4	846	2	09C1O1	09c1o1 lactococcus	1075	67	7.4	552	2	065XU0	065xu0 oryza sativ
1003	67.5	7.4	851	2	08L613	08l613 arabidopsis	1076	67	7.4	564	2	06NTE7	06nte7 homo sapien
1004	67.5	7.4	916	2	09YXK8	09yxk8 neisseria m	1077	67	7.4	592	2	08ERD5	08erd5 oceanobacil
1005	67.5	7.4	929	2	075QNG	075qng arabidopsis	1078	67	7.4	600	2	07YZB8	07yzb8 tenebrio mo
1006	67.5	7.4	946	2	09FFA8	09ffa8 candida gla	1079	67	7.4	600	2	0701L8	0701l8 homo sapien
1007	67.5	7.4	959	2	06FT79	06ft79 arabidopsis	1080	67	7.4	600	2	06T721	06t721 brachydanio
1008	67.5	7.4	989	2	023723	023723 arabidopsis	1081	67	7.4	613	2	093JN4	093jn4 xanthomonas
1009	67.5	7.4	1005	2	093708	093708 escherichia	1082	67	7.4	618	2	07UZ24	07uz24 prochloroc
1010	67.5	7.4	1108	2	0817E8	0817e8 bacillus ce	1083	67	7.4	628	2	07XV05	07xv05 oryza sativ
1011	67.5	7.4	1130	2	08CFE5	08cfe5 mus musculu	1084	67	7.4	629	1	K2C3_HUMAN	k2c3_human
1012	67.5	7.4	1138	2	022276	022276 caenorhabdi	1085	67	7.4	639	2	09SFF4	09sff4 arabidopsis
1013	67.5	7.4	1140	2	069ZW5	069zw5 mus musculu	1086	67	7.4	634	2	094KA5	094ka5 picea abies
1014	67.5	7.4	1191	1	CING_MOUSE	ps9242 mus musculu	1087	67	7.4	639	2	09XH26	09xh26 arabidopsis
1015	67.5	7.4	1223	2	06P2K0	06p2k0 mus musculu	1088	67	7.4	671	2	07QJ04	07qj04 anopheles g
1016	67.5	7.4	1240	2	069ZM0	069zm0 mus musculu	1089	67	7.4	701	2	06A9K7	06a9k7 propionibac
1017	67.5	7.4	1258	2	06B8G6	06b8g6 paramecium	1090	67	7.4	763	2	06BK65	06bk65 debaryomyce
1018	67.5	7.4	1287	2	07Z362	07z362 homo sapien	1091	67	7.4	790	2	06BJ29	06bj29 pseudomonas
1019	67.5	7.4	1509	2	07QOP8	07qop8 giardia lam	1092	67	7.4	824	2	081JDO	081jdo bacillus ce
1020	67.5	7.4	1572	2	06MJT8	06mjt8 bdellovibri	1093	67	7.4	833	2	086V65	086v65 homo sapien
1021	67.5	7.4	1624	2	09W4J7	09w4j7 drosophila	1094	67	7.4	844	2	06C9T4	06c9t4 yarrowia li
1022	67.5	7.4	1964	2	093522	093522 xenopus lae	1095	67	7.4	856	2	08WV98	08wv98 homo sapien
1023	67.5	7.4	2077	2	06WMN2	06wmn2 neurospora	1096	67	7.4	857	2	0887K8	0887k8 pseudomonas
1024	67.5	7.4	3175	2	07JKT8	07jkt8 caenorhabdi	1097	67	7.4	861	2	08BO74	08bo74 m mus muscu
1025	67.5	7.4	3184	2	09XV66	09xv66 caenorhabdi	1098	67	7.4	872	2	09P221	09p221 homo sapien
1026	67.5	7.4	6885	1	SNE2_HUMAN	064hnt4 bacterioph	1099	67	7.4	888	2	068DH6	068dh6 homo sapien
1027	67	7.4	118	2	064HN4	064hnt4 bacterioph	1100	67	7.4	891	1	09SUX9	09sux9 arabidopsis
1028	67	7.4	118	2	064HN6	064hnt6 bacterioph	1101	67	7.4	928	1	NIBA_HUMAN	niba_human
1029	67	7.4	153	2	073KS0	073ks0 treponema d	1102	67	7.4	931	2	09UXV7	09uxv7 pyrococcus
1030	67	7.4	172	2	093VL3	093vl3 phaseolus v	1103	67	7.4	941	2	028662	028662 oryza sativ
1031	67	7.4	180	2	07XBV8	07xbv8 oryza sativ	1104	67	7.4	941	2	09TS14	09ts14 oryza sativ
1032	67	7.4	207	2	09AVL7	09avl7 oryza sativ	1105	67	7.4	945	2	06L465	06l465 solanum dem
1033	67	7.4	280	1	RS4_BORPE	rs4b774 bordetella	1106	67	7.4	1008	2	08YQ48	08yq48 anabaena ep
1034	67	7.4	234	1	B1OD_BACSH	p22818 bacillus sp	1107	67	7.4	1047	2	066QA6	066qa6 oryza sativ
1035	67	7.4	237	2	083L34	083l34 shigelila fl	1108	67	7.4	1066	1	SYI_PYRHO	syi_pyrho
1036	67	7.4	264	2	022027	022027 caenorhabdi	1109	67	7.4	1106	2	09PMD0	09pmd0 tetraodon f
1037	67	7.4	266	2	06HMT2	06hmt2 bacillus an	1110	67	7.4	1126	2	073ME8	073me8 treponema d
1038	67	7.4	270	2	08DH81	08dh81 vibrio vuln	1111	67	7.4	1128	2	07SKX2	07skx2 brachydanio
1039	67	7.4	283	2	08DA83	08da83 vibrio vuln	1112	67	7.4	1154	2	068XK6	068xk6 ticketella
1040	67	7.4	287	2	08MRP1	08mrp1 caenorhabdi	1113	67	7.4	1158	2	086H52	086h52 dictyosteli
1041	67	7.4	293	2	066666	066666 aquilex aeo	1114	67	7.4	1235	1	KPB2_MOUSE	kpb2_mouse
1042	67	7.4	303	2	08BHV4	08bhv4 mus musculu	1115	67	7.4	1241	1	KPB1_MOUSE	kpb1_mouse
1043	67	7.4	316	2	06MBD7	06mbd7 parachlamyd	1116	67	7.4	1242	2	0824R6	0824r6 chlamydomphi
1044	67	7.4	317	2	06J0Y5	06j0y5 parallelchth	1117	67	7.4	1278	2	050667	050667 borella bu
1045	67	7.4	329	2	075JW2	075jw2 arabhya goss	1118	67	7.4	1283	2	0815R4	0815r4 plasmodium
1046	67	7.4	336	2	08WZL6	08wzl6 yarrowia li	1119	67	7.4	1292	2	06C910	06c910 yarrowia li
1047	67	7.4	336	2	06C3B1	06c3b1 yarrowia li	1120	67	7.4	1632	2	084KC9	084kc9 hordeum vul
1048	67	7.4	365	2	079JBI	079jel corynebacte	1121	67	7.4	1739	2	06ZE11	06ze11 oryza sativ
1049	67	7.4	365	2	08NTG4	08ntg4 corynebacte	1122	67	7.4	1805	1	HMM2_MYCGE	hmm2_mycge
1050	67	7.4	391	2	097Y44	097y44 sulfolobus	1123	67	7.4	1863	2	07XT09	07xt09 oryza sativ
1051	67	7.4	410	2	07VLG7	07vlg7 haemophilus	1124	67	7.4	2094	2	080Y35	080y35 mus musculu
1052	67	7.4	411	2	0873M8	0873m8 mucor circi	1125	67	7.4				
1053	67	7.4	421	2	08XP15	08xp15 talatonia s	1126	67	7.4				

1127	67	7.4	2182	2	0811T5	0811z5	plasmidium	1200	66.5	7.3	875	2	0723V3	Q723v3	homo sapien
1128	67	7.4	2527	2	095W83	095w83	treponema	1201	66.5	7.3	876	2	078E87	Q78E87	mus musculus
1129	67	7.4	3320	2	073MF0	073mf0	respiromon d	1202	66.5	7.3	880	1	TYO3_MOUSE	P55144	mus musculus
1130	67	7.4	4624	1	DYH5_HUMAN	08e7z3	homo sapien	1203	66.5	7.3	880	1	TYO3_CAT	P55146	rattus norv
1131	66.5	7.3	144	2	096MK1	096mk1	homo sapien	1204	66.5	7.3	880	2	06VZM6	06vzm6	mus musculus
1132	66.5	7.3	211	2	06Q8W4	06q8w4	uncultured	1205	66.5	7.3	886	1	VP39_HUMAN	0961j1	homo sapien
1133	66.5	7.3	264	2	08WVG2	08wvg2	homo sapien	1206	66.5	7.3	894	2	06DD73	06dd73	xenopus lae
1134	66.5	7.3	279	2	064UP9	064up9	bacteroides	1207	66.5	7.3	916	2	09JTK7	09jtk7	neisseria r
1135	66.5	7.3	287	2	064Y62	064y62	bacteroides	1208	66.5	7.3	923	2	081Q08	081q08	drosophila
1136	66.5	7.3	292	2	06ASE4	06ase4	denulfotale	1209	66.5	7.3	950	2	095N28	095n28	dictyostelli
1137	66.5	7.3	303	2	081A70	081a70	bacillus ce	1210	66.5	7.3	960	2	081B56	081b56	bacillus ce
1138	66.5	7.3	333	2	07V472	07v472	prochloroc	1211	66.5	7.3	1037	2	06GL13	06gl13	xenopus ttr
1139	66.5	7.3	341	2	073515	073515	bacillus ce	1212	66.5	7.3	1081	2	08BMA5	08bma5	mus muscul
1140	66.5	7.3	342	2	07V432	07v432	prochloroc	1213	66.5	7.3	1107	2	07ZD23	07zd23	bacillus ce
1141	66.5	7.3	350	2	07PST5	07pst5	atrophelae g	1214	66.5	7.3	1110	2	09SUZ3	09su23	arabidopsis
1142	66.5	7.3	357	2	096D17	096d17	homo sapien	1215	66.5	7.3	1121	2	07QXU5	07qxj5	giardia lam
1143	66.5	7.3	358	2	06PR01	06pe01	mus musculu	1216	66.5	7.3	1128	2	07UD84	07ude4	shigella fl
1144	66.5	7.3	360	2	064BP4	064bp4	uncultured	1217	66.5	7.3	1195	2	09C730	09c730	arabidopsis
1145	66.5	7.3	362	2	08A7L9	08a7l9	bacteroides	1218	66.5	7.3	1198	2	06FDP6	06fdp6	acinetobact
1146	66.5	7.3	381	2	08ANE4	08ney4	homo sapien	1219	66.5	7.3	1246	2	09C6D9	09c6d9	arabidopsis
1147	66.5	7.3	382	1	096EL8	096el8	homo sapien	1220	66.5	7.3	1363	2	065XW3	065xw3	oryza sativ
1148	66.5	7.3	382	1	TGT_HAEIN	P44594	haemophilu	1221	66.5	7.3	1504	2	065XW3	091kx4	arabidopsis
1149	66.5	7.3	392	2	08TCQ4	08tcq4	homo sapien	1222	66.5	7.3	1728	2	09LUT4	09lut4	arabidopsis
1150	66.5	7.3	401	2	07SB17	07sbt7	abhyda goss	1223	66.5	7.3	1833	2	08OT68	08ot68	mus musculu
1151	66.5	7.3	406	2	09FJ17	09fj17	arabidopsis	1224	66.5	7.3	1976	1	MHA_BOVIN	027901	bos taurus
1152	66.5	7.3	412	2	08AVX9	08avx9	xenopus lae	1225	66.5	7.3	2202	2	06BPL1	06bpl1	debarryomyce
1153	66.5	7.3	428	2	06P8E8	06p8e8	xenopus tro	1226	66.5	7.3	2217	2	06FNY7	06fny7	candida gla
1154	66.5	7.3	433	2	052160	052160	plasmid pes	1227	66	7.3	1119	2	09XZ82	09xz82	plasmidium
1155	66.5	7.3	439	2	08YK82	08yk82	anabaena sp	1228	66	7.3	158	2	08YVBO	08yvbo	anabaena sp
1156	66.5	7.3	439	2	07U3U0	07u3u0	synecchococ	1229	66	7.3	160	1	COAD_CORGL	08hqu5	corynebacte
1157	66.5	7.3	446	2	08VXD4	08vxd4	nicotiana t	1230	66	7.3	177	2	072680	06S941	bean dwarf
1158	66.5	7.3	446	2	09ST97	09st97	nicotiana t	1231	66	7.3	180	2	06S941	06S941	plasmidium
1159	66.5	7.3	455	2	08BHx2	08bhx2	pseudomonas	1232	66	7.3	208	2	07PMO3	07pmq3	anophelae g
1160	66.5	7.3	455	2	08BHx2	08bhx2	pseudomonas	1232	66	7.3	210	2	08VTP2	08vtp2	helicobacte
1161	66.5	7.3	494	1	WD37_HUMAN	Q9Y218	homo sapien	1233	66	7.3	210	2	08VTP3	08vtp3	helicobacte
1162	66.5	7.3	513	1	VGA_BPPIX	P03631	bacterioph	1234	66	7.3	214	1	Y629_METUA	049351	arabidopsis
1163	66.5	7.3	513	1	Q71A13	Q71a13	anaplasma m	1235	66	7.3	234	1	049351	049351	arabidopsis
1164	66.5	7.3	534	1	YF84_STRP6	P67283	streptococc	1237	66	7.3	237	2	09XKH9	09xkh9	bacillus ha
1165	66.5	7.3	534	1	YH39_STRP6	P67283	streptococc	1238	66	7.3	237	2	09XKH9	09xkh9	bacillus ha
1166	66.5	7.3	562	1	CH60_TRYCR	Q95046	trypanosoma	1239	66	7.3	258	2	Q55376	Q55376	synecchocyc
1167	66.5	7.3	563	1	YMO3_CAEEL	Q10906	caenorhabd1	1240	66	7.3	259	2	Q41533	Q41533	criticum ae
1168	66.5	7.3	568	1	06CAHO	06caho	erwinia ll	1241	66	7.3	270	2	Q7MM15	Q7mm15	vibrio vuln
1169	66.5	7.3	575	2	06D6D6	06d6d6	erwinia car	1242	66	7.3	272	2	0847U9	0847u9	vibrio para
1170	66.5	7.3	581	2	06EBB6	06ebb6	campylobact	1243	66	7.3	277	2	087GA7	087ga7	vibrio para
1171	66.5	7.3	597	2	091871	091871	xenopus lae	1245	66	7.3	287	2	09XX63	09xx63	caenorhabd1
1172	66.5	7.3	600	2	09PHW8	09phw8	campylobact	1245	66	7.3	289	2	Q7QBR3	Q7qbr3	anophelae g
1173	66.5	7.3	608	2	0603J8	0603j8	homo sapien	1246	66	7.3	332	2	08VMK6	08vmk6	pseudomonas
1174	66.5	7.3	608	2	06K3B8	06k3b8	oryza sativ	1247	66	7.3	332	2	08VUH7	08vuh7	pseudomonas
1175	66.5	7.3	629	2	094HU4	094hu4	oryza sativ	1248	66	7.3	332	2	08H1L7	08h1l7	pseudomonas
1176	66.5	7.3	633	2	09H094	09h094	homo sapien	1249	66	7.3	337	2	09MWY4	09mw4	pseudomonas
1177	66.5	7.3	636	2	035656	035656	mus musculu	1250	66	7.3	340	1	PPTA_ARATH	Q91XJ3	a protein f
1178	66.5	7.3	641	2	08WMT4	08wmt4	homo sapien	1251	66	7.3	344	1	06C6W3	Q6c6w3	yarrowia ll
1179	66.5	7.3	643	2	06P3X9	06p3x9	homo sapien	1252	66	7.3	361	2	06AGP6	Q6agp6	leifsonia x
1180	66.5	7.3	652	2	08IM59	08im59	plasmodium	1253	66	7.3	363	2	098321	098321	hymenasplen
1181	66.5	7.3	658	2	0631I6	0631i6	bacillus ce	1254	66	7.3	374	1	08BECM3	08bcm3	shewanella
1182	66.5	7.3	658	2	072XV1	072xv1	bacillus ce	1255	66	7.3	375	1	TGT_ECOLI	P19675	escherichia
1183	66.5	7.3	658	2	081513	081513	bacillus ce	1256	66	7.3	375	1	TGT_SHIFL	Q54177	shigella fl
1184	66.5	7.3	658	2	081X47	081x47	bacillus an	1257	66	7.3	375	2	08RBT1	Q8rbt1	thermoanaer
1185	66.5	7.3	658	2	06HBC2	06hbc2	bacillus th	1258	66	7.3	386	2	083V39	083v39	pseudomonas
1186	66.5	7.3	666	2	064XN8	064xn8	bacteroides	1259	66	7.3	399	2	Q21342	Q21342	caenorhabd1
1187	66.5	7.3	677	2	06HP67	06hp67	bacillus th	1260	66	7.3	414	2	Q36857	Q36857	xiphopteris
1188	66.5	7.3	679	2	08B8G5	08b8g5	shewanella	1261	66	7.3	424	2	06ALC7	Q6alc7	denulfotale
1189	66.5	7.3	681	2	08KPY1	08kpy1	synecchococ	1262	66	7.3	434	2	0913S6	Q913s6	anabaena sp
1190	66.5	7.3	684	2	06DE20	06de20	xenopus lae	1263	66	7.3	437	1	LHA2_HUMAN	Q00534	homo sapien
1191	66.5	7.3	735	2	08WGU6	08wgu6	penantia c	1264	66	7.3	467	2	06GR24	Q6gr24	xenopus lae
1192	66.5	7.3	745	2	06PCF2	06pcf2	xenopus lae	1265	66	7.3	470	2	P94053	P94053	plocama pen
1193	66.5	7.3	763	2	08WMS6	08wms6	homo sapien	1266	66	7.3	475	2	08H6M1	Q8hm61	sema2ophy11
1194	66.5	7.3	771	2	09BVJ6	09bvj6	homo sapien	1267	66	7.3	475	2	033631	033631	streptococc
1195	66.5	7.3	793	2	084TB4	084tb4	oryza sativ	1268	66	7.3	479	2	08EAB9	Q8eab9	shewanella
1196	66.5	7.3	832	1	TRNL_CANAL	P43075	candida alb	1269	66	7.3	492	1	KCCO_CHICK	Q93532	gallus gall
1197	66.5	7.3	837	2	06PB65	06pb65	mus musculu	1270	66	7.3	498	2	06CZD8	Q6czd8	erwinia car
1198	66.5	7.3	867	2	081210	081210	arabidopsis	1271	66	7.3	499	1	NIFB_BRADJA	P06770	bradyrhizob
1199	66.5	7.3	875	2	071506	071506	homo sapien	1272	66	7.3	503	2	Q95LY0	Q95ly0	macaca fasc

1273	66	7.3	514	2	Q80VD9	Q80vd9 mus musculus	1346	65.5	7.2	206	1	RS4_PHOIL	Q7myh4 photorhabdu
1274	66	7.3	540	2	Q6MFA7	Q6mfat parachlamy	1347	65.5	7.2	206	2	Q65QX9	Q65qx9 manheimia
1275	66	7.3	553	2	Q9KC39	Q9kc39 bacillus ha	1348	65.5	7.2	223	2	Q6PH25	Q6ph25 brachydanio
1276	66	7.3	554	2	Q36X04	Q36x04 podospora a	1349	65.5	7.2	228	2	Q836F9	Q836f9 enterococcu
1277	66	7.3	562	1	EZRA_BACSU	Q34894 bacillus su	1350	65.5	7.2	249	1	PSB2_THETN	Q8r912 thermoaer
1278	66	7.3	566	2	Q7X3P9	Q7x3p9 staphylococ	1351	65.5	7.2	252	2	Q99V78	Q99v78 staphylococ
1279	66	7.3	573	2	Q6E1N1	Q6e1n1 bacillus sp	1352	65.5	7.2	252	2	Q7A199	Q7a199 staphylococ
1280	66	7.3	573	2	Q6E1N6	Q6e1n6 geobacillus	1353	65.5	7.2	252	2	Q7A6D5	Q7a6d5 staphylococ
1281	66	7.3	575	2	Q6P6Q2	Q6p6q2 rattus norv	1354	65.5	7.2	252	2	Q6GAR3	Q6gar3 staphylococ
1282	66	7.3	576	2	Q6P6Q2	Q6p6q2 rattus norv	1355	65.5	7.2	252	2	Q6GAR3	Q6gar3 staphylococ
1283	66	7.3	576	2	Q7TN87	Q7tn87 rattus norv	1356	65.5	7.2	256	2	Q8C3X2	Q8c3x2 mus musculu
1284	66	7.3	600	2	Q9ET74	Q9et74 mus musculu	1356	65.5	7.2	256	2	Q9D7C1	Q9d7c1 mus musculu
1285	66	7.3	644	2	Q7J3E11	Q7j3e11 bacillus ce	1357	65.5	7.2	285	2	Q6D8A2	Q6d8a2 xenopus lae
1286	66	7.3	650	2	Q6F9S7	Q6f9s7 acinetobact	1358	65.5	7.2	289	2	Q75BV1	Q75bv1 ashbya gos
1287	66	7.3	685	2	Q8D465	Q8d465 vibrio vuln	1359	65.5	7.2	289	2	Q8A6H6	Q8a6h6 bacteroides
1287	66	7.3	716	2	Q7MP22	Q7mp22 vibrio vuln	1360	65.5	7.2	300	1	SP18_YEAST	P32572 saccharomyc
1288	66	7.3	729	1	PCRA_STAEP	Q8cte8 staphylococ	1361	65.5	7.2	328	1	AIPL_MOUSE	Q924k1 mus musculu
1289	66	7.3	730	2	Q87JC8	Q87jc8 neurospora	1362	65.5	7.2	332	1	Q8Q853	Q8q853 human immun
1290	66	7.3	781	2	Q6NUJ2	Q6nuj2 xenopus lae	1363	65.5	7.2	333	2	Q8KSX2	Q8ksx2 streptomyc
1291	66	7.3	786	1	STSB_MOUSE	P42232 mus musculu	1364	65.5	7.2	351	2	Q8Z2S0	Q8z2s0 salmonella
1292	66	7.3	786	1	STSB_RAT	P52632 rattus norv	1365	65.5	7.2	351	2	Q8ZLF0	Q8zlf0 salmonella
1293	66	7.3	786	2	Q6UNT9	Q6unt9 homo sapien	1366	65.5	7.2	353	2	Q6ZRL4	Q6zrl4 homo sapien
1294	66	7.3	786	2	Q8K3Q1	Q8k3q1 mus musculu	1367	65.5	7.2	364	1	YBBB_ECOLI	P33667 escherichia
1295	66	7.3	786	2	Q9UKM1	Q9ukm1 mus musculu	1368	65.5	7.2	364	2	Q8XCZ2	Q8xcz2 escherichia
1296	66	7.3	791	2	Q8WMS9	Q8wms9 homo sapien	1369	65.5	7.2	366	2	Q7Q0Z1	Q7q0z1 anopheles g
1297	66	7.3	794	1	STSA_HUMAN	P42229 homo sapien	1370	65.5	7.2	371	2	Q6E130	Q6e130 synechococc
1298	66	7.3	799	2	Q6BLI8	Q6bli8 debaryomyce	1371	65.5	7.2	372	2	Q93QJ3	Q93qj3 salmonella
1299	66	7.3	805	2	Q6RK13	Q6rk13 parietaria	1372	65.5	7.2	372	2	Q455Q6	Q455q6 bacillus su
1300	66	7.3	812	2	Q9ASG7	Q9asg3 oryza sativ	1373	65.5	7.2	372	2	Q9S522	Q9s522 escherichia
1301	66	7.3	846	2	Q9C9H7	Q9c9h7 arabidopsis	1374	65.5	7.2	375	1	TGT_SALTI	Q8z8y0 salmonella
1302	66	7.3	846	2	Q9PN76	Q9pn76 campylobact	1375	65.5	7.2	375	2	Q97EW2	Q97ew2 clostridium
1303	66	7.3	853	1	PHS1_DICDI	Q00766 dictyosteli	1376	65.5	7.2	377	2	Q72UJ3	Q72uj3 leptospira
1304	66	7.3	867	2	Q6AXB4	Q6axb4 mus musculu	1377	65.5	7.2	378	2	Q8YUW5	Q8yuw5 anabaena sp
1305	66	7.3	922	2	Q8TCY9	Q8tcy9 homo sapien	1378	65.5	7.2	380	2	Q63QX3	Q63qx3 burkholderi
1306	66	7.3	1018	2	Q9HCT1	Q9hct1 homo sapien	1379	65.5	7.2	384	2	Q7QKN1	Q7qkn1 anopheles g
1307	66	7.3	1028	2	Q6YR24	Q6yr24 onion yello	1380	65.5	7.2	387	2	Q9X941	Q9x941 streptomyc
1308	66	7.3	1031	1	KINH_STRPU	P35978 strongyloce	1381	65.5	7.2	404	1	FGK_MYCMS	P62415 mycoplasma
1309	66	7.3	1047	1	Q67IT5	Q67it5 oryza sativ	1382	65.5	7.2	405	2	Q9M2V1	Q9m2v1 arabidopsis
1310	66	7.3	1050	1	HER3_HUMAN	Q15034 homo sapien	1383	65.5	7.2	424	2	Q8B6C5	Q8b6c5 pseudomonas
1311	66	7.3	1052	2	Q91G49	Q91g49 chilo tride	1384	65.5	7.2	430	1	FOLC_BACSU	Q05865 bacillus su
1312	66	7.3	1099	2	Q6FV36	Q6fv36 candida gla	1385	65.5	7.2	431	1	SGK1_RABIT	Q9xtl8 cryptococcus
1313	66	7.3	1160	2	Q6NX72	Q6nx72 homo sapien	1386	65.5	7.2	431	2	Q7V3V9	Q7v3v9 prochloroco
1314	66	7.3	1181	2	Q9KN45	Q9kn45 vibrio chol	1387	65.5	7.2	446	2	Q8VD23	Q8vd23 mus musculu
1315	66	7.3	1199	2	Q8NM7	Q8nm7 homo sapien	1388	65.5	7.2	451	2	Q89VS8	Q89vs8 bradyrhizob
1316	66	7.3	1274	2	Q8NFR0	Q8nfr0 homo sapien	1389	65.5	7.2	463	1	YRB3_CABEL	Q09400 caenorhabdi
1317	66	7.3	1289	2	Q62717	Q62717 rattus norv	1390	65.5	7.2	465	2	Q9U1S3	Q9u1s3 caenorhabdi
1318	66	7.3	1318	2	Q6FTJ2	Q6ftj2 candida gla	1391	65.5	7.2	471	2	Q85YMO	Q85ymo monadenium
1319	66	7.3	1336	2	Q7R3R6	Q7r3r6 giardia lam	1392	65.5	7.2	483	2	Q7NIG0	Q7nig0 glieobacter
1320	66	7.3	1382	2	Q61374	Q61374 mus musculu	1393	65.5	7.2	484	2	Q63G58	Q63g58 bacillus ce
1321	66	7.3	1383	2	Q9VDA0	Q9vda0 drosophila	1394	65.5	7.2	486	2	Q8FHD0	Q8fhd0 escherichia
1322	66	7.3	1390	2	Q9UL08	Q9ul08 homo sapien	1395	65.5	7.2	486	2	Q83R89	Q83r89 shigella fl
1323	66	7.3	1392	2	Q80TV1	Q80tv1 mus musculu	1396	65.5	7.2	496	2	Q8Y649	Q8y649 listeria mo
1324	66	7.3	1610	2	Q74349	Q74349 schizosacch	1397	65.5	7.2	509	2	Q7UHA1	Q7uha1 rhodospirell
1325	66	7.3	1732	2	Q7QDU1	Q7qdu1 anopheles g	1398	65.5	7.2	531	2	Q7Y205	Q7y205 cryptospori
1326	66	7.3	1953	1	BN11_YEAST	P41832 saccharomyc	1399	65.5	7.2	540	2	Q8D8W2	Q8d8w2 vibrio vuln
1327	66	7.3	2013	2	Q9VK10	Q9vk10 drosophila	1400	65.5	7.2	542	2	Q7MLI0	Q7ml10 vibrio vuln
1328	66	7.3	2030	1	NIN_HUMAN	Q9n4c6 homo sapien	1401	65.5	7.2	543	2	Q9QO15	Q9qo15 influenza a
1329	66	7.3	2244	2	Q9NCG0	Q9ncg0 drosophila	1402	65.5	7.2	545	2	Q88B36	Q88b36 mus musculu
1330	66	7.3	2282	2	Q6CAD2	Q6cad2 varrovia li	1403	65.5	7.2	545	2	Q6ZTE7	Q6zte7 homo sapien
1331	66	7.3	2326	2	Q8IIV6	Q8iiv6 plasmodium	1404	65.5	7.2	566	2	Q32239	Q32239 bacillus su
1332	66	7.3	2524	1	NOTC_XENLA	P21783 xenopus lae	1405	65.5	7.2	569	2	Q8LNV6	Q8lnv6 oryza sativ
1333	66	7.3	3265	2	Q8ID63	Q8id63 plasmodium	1406	65.5	7.2	576	2	Q83SE9	Q83se9 shigella fl
1334	66	7.3	4264	2	Q8T3P1	Q8t3p1 anopheles g	1407	65.5	7.2	600	2	Q91ZJ7	Q91zj7 mus musculu
1335	66	7.2	114	2	Q8T327	Q8t327 plasmodium	1408	65.5	7.2	621	2	Q6NSU0	Q6nsc0 mus musculu
1336	65.5	7.2	126	2	Q9MZF8	Q9mzf8 mecaca mula	1409	65.5	7.2	624	2	Q6S7F1	Q6s7f1 oryza sativ
1337	65.5	7.2	151	2	Q6S8V1	Q6s8v1 plasmodium	1410	65.5	7.2	624	2	Q6Z4U4	Q6z4u4 oryza sativ
1338	65.5	7.2	151	2	Q6HIE8	Q6hie8 bacillus th	1411	65.5	7.2	626	2	Q8IRK3	Q8irk3 drosophila
1339	65.5	7.2	182	2	Q67BJ6	Q67bj6 ovine herpe	1412	65.5	7.2	677	2	Q7RR19	Q7rr19 plasmodium
1340	65.5	7.2	183	2	Q8DWM7	Q8dwm7 streptococc	1413	65.5	7.2	674	2	Q7ZBNO	Q7zbn0 desulfovibtr
1341	65.5	7.2	183	2	Q8E2R8	Q8e2r8 streptococc	1414	65.5	7.2	689	2	P87565	P87565 canine aden
1342	65.5	7.2	199	2	Q8R505	Q8r505 mus musculu	1415	65.5	7.2	694	2	Q751Y8	Q751y8 ashbya gos
1343	65.5	7.2	205	1	RS4_HAEIN	P44373 haemophilus	1416	65.5	7.2	706	2	Q8BXK3	Q8bxk3 mus musculu
1344	65.5	7.2	206	1	RS4_BUCBP	P59491 buchiera ap	1417	65.5	7.2	716	2	Q7QK23	Q7qk23 anopheles g
1345	65.5	7.2	206	1	RS4_PASMU	Q9c153 pasteurella	1418	65.5	7.2	745	1	CUL2_HUMAN	Q13617 homo sapien

1419	65.5	7.2	745	1	CUL2, MOUSE	O6q4h6 mus musculus
1420	65.5	7.2	756	2	O69D70	O69d70 oryza sativ
1421	65.5	7.2	777	2	O81G16	O81g16 bacillus ce
1422	65.5	7.2	798	2	O8BUJ2	O8buJ2 mus musculus
1423	65.5	7.2	803	2	O9CB85	O9cb85 mycobacteri
1424	65.5	7.2	811	2	O6G1Q8	O6g1q8 bartonella
1425	65.5	7.2	821	2	P72351	P72351 mycobacteri
1426	65.5	7.2	826	2	O6FPN1	O6fFn1 actinobact
1427	65.5	7.2	845	1	AMPN_LALIC	P3J897 lactococcus
1428	65.5	7.2	875	2	O8BY36	O8by36 mus musculus
1429	65.5	7.2	886	1	VP39, MOUSE	O8r513 mus musculus
1430	65.5	7.2	913	2	O12151	O12151 saccharomyc
1431	65.5	7.2	932	2	O9CEH8	O9ceH8 lactococcus
1432	65.5	7.2	940	2	O35157	O35157 mus musculus
1433	65.5	7.2	944	2	O829N2	O829n2 salmoneila
1434	65.5	7.2	944	2	O82R20	O82r20 salmoneila
1435	65.5	7.2	958	2	O68FLO	O68f10 mus musculus
1436	65.5	7.2	969	2	O8N3W0	O8n3w0 homo sapien
1437	65.5	7.2	970	1	NA01, MOUSE	P70414 mus musculus
1438	65.5	7.2	983	2	O9QXN1	O9qxm1 mus musculus
1439	65.5	7.2	988	2	O6BTB2	O6btb2 homo sapien
1440	65.5	7.2	1012	2	O6CYH4	O6cyh4 kluyveromyc
1441	65.5	7.2	1013	2	O85920	O85920 spingomonas
1442	65.5	7.2	1015	2	O8YVPA	O8yvpa anabaena sp
1443	65.5	7.2	1038	2	O7OD58	O7ods8 anopheles g
1444	65.5	7.2	1060	2	O72X11	O72x11 xenopus lae
1445	65.5	7.2	1061	2	O69YK7	O69yk7 homo sapien
1446	65.5	7.2	1063	2	O81WFA	O81wf4 homo sapien
1447	65.5	7.2	1063	2	O8N4O6	O8n4o6 homo sapien
1448	65.5	7.2	1088	2	O00905	O00905 oxytricha f
1449	65.5	7.2	1115	2	O17267	O17267 caenorhabdi
1450	65.5	7.2	1130	2	O81TY8	O81ty8 caenorhabdi
1451	65.5	7.2	1133	2	O81949	O81949 anopheles g
1452	65.5	7.2	1153	2	O6B1P2	O6b1p2 debaryomyc
1453	65.5	7.2	1157	2	O897P5	O897p5 clostridium
1454	65.5	7.2	1164	1	TS01, HUMMAN	O92574 homo sapien
1455	65.5	7.2	1186	2	O6FW19	O6fw19 candida gla
1456	65.5	7.2	1197	2	O9B121	O9b121 drosophila
1457	65.5	7.2	1197	2	O9VCB8	O9vcB8 drosophila
1458	65.5	7.2	1203	2	O6PFK8	O6pfk8 brachydanio
1459	65.5	7.2	1204	2	O75A42	O75a42 aabhyas goss
1460	65.5	7.2	1227	2	O70OK7	O70ok7 anopheles g
1461	65.5	7.2	1275	2	O6Z3S5	O6z3s5 oryza sativ
1462	65.5	7.2	1415	2	O9HCF4	O9hcf4 homo sapien
1463	65.5	7.2	1487	1	NU0B_VIBPA	O8tqw2 vibrio para
1464	65.5	7.2	1509	2	O6BT40	O6bt40 homo sapien
1465	65.5	7.2	1681	2	O6MBY1	O6mbY1 paracalamyd
1466	65.5	7.2	1785	2	O9N8T7	O9n8t7 trypanosoma
1467	65.5	7.2	1855	2	O6ZPL0	O6zpl0 mus musculus
1468	65.5	7.2	1866	1	VCNB, CPWV	P03600 compea mosca
1469	65.5	7.2	2101	2	O14981	O14981 homo sapien
1470	65.5	7.2	2115	1	N1MA, HUMMAN	O14980 homo sapien
1471	65.5	7.2	2296	2	O75O42	O75o42 homo sapien
1472	65.5	7.2	3139	2	O9GM99	O9gm99 sus scrofa
1473	65.5	7.2	3152	2	O8U237	O8u237 leek yellow
1474	65.5	7.2	3397	2	O8UW79	O8uw79 galus galli
1475	65.5	7.2	4390	2	O9VZ77	O9vz77 drosophila
1476	65.5	7.2	5229	2	O7RTF4	O7rtf4 plasmodium
1477	65.5	7.2	104	2	O79Y28	O79y28 streptococc
1478	65.5	7.2	105	2	O880J3	O880j3 pseudomona
1479	65.5	7.2	156	2	O9FN29	O9fn29 arabidopsis
1480	65.5	7.2	157	2	O8RGQ3	O8rgq3 thermotaneer
1481	65.5	7.2	159	2	O90308	O90308 cotton yell
1482	65.5	7.2	190	2	O8WTD8	O8wtd8 plasmodium
1483	65.5	7.2	206	2	O7NBT7	O7nbt7 mycoplasma
1484	65.5	7.2	210	1	THAI, MOUSE	O8chw1 mus musculus
1485	65.5	7.2	210	2	O9PBE8	O9pbe8 helicobacte
1486	65.5	7.2	220	1	KAD_PRRAB	O9zn1 pyrococcus
1487	65.5	7.2	221	2	O7TF12	O7tf12 ribesue cyto
1488	65.5	7.2	222	2	O9LWV6	O9lwv6 arabidopsis
1489	65.5	7.2	222	2	O841M5	O841m5 streptomyc
1490	65.5	7.2	236	2	O46248	O46248 clostridium
1491	65.5	7.2	240	2	O8NKK5	O8nkk5 uncultured

1492	65	7.2	251	2	O8QMH8	O8qmh8 sida motile
1493	65	7.2	251	2	O70PC3	O70pc3 sida micran
1494	65	7.2	254	2	O91307	O91307 rana catesb
1495	65	7.2	265	2	O6Y217	O6y217 pagrus majo
1496	65	7.2	277	2	O7PS09	O7ps09 anopheles g
1497	65	7.2	280	2	O25846	O25846 plasmodium
1498	65	7.2	280	2	O25855	O25855 plasmodium
1499	65	7.2	291	2	O8PV67	O8pv67 methanosarc
1500	65	7.2	291	2	O63Hm6	O63hm6 homo sapien

ALIGNMENTS

RESULT 1
INT1_SHEEP
ID INT1_SHEEP STANDARD; PRT; 195 AA.
AC P56828; P08316;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interferon tau-1 precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
DE (Trophoblastin) (Antileucystin) (Trophoblast antileucolytic protein).
GN Name=IFNT1; Synonyms=OTF;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Trophoblast;
RX MEDLINE=88065855; PubMed=2446135; DOI=10.1038/330377a0;
RA Imakawa K., Antony R.V., Kazemi M., Marotti K.R., Polites H.G.,
RT Roberts R.M.;
RT "Interferon-like sequence of ovine trophoblast protein secreted by
RT embryonic trophoblast";
RL Nature 330:377-379(1987).
RN [2]
RN FUNCTION.
RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
RA Spencer T.E., Bazer F.W.;
RT "Ovine interferon tau suppresses transcription of the estrogen
RT receptor and oxytocin receptor genes in the ovine endometrium";
RL Endocrinology 137:1144-1147(1996).
RN [3]
RN CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
RX MEDLINE=95062134; PubMed=7971949;
RA Jarpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curto E.V.,
RA Krishna N.R., Pontzer C.H.;
RT "Predicted structural motif of IFN tau";
RL Protein Eng. 7:863-867(1994).
RN [4]
RN 3D-STRUCTURE MODELING.
RX MEDLINE=96318252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [5]
RN REVIEW.
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.-L., Chene N.M., Huynh L.P., V'Hardon R.M., Reinard P.B.,
RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT potentialities";
RL Biochimie 80:755-777(1998).
CC -i- FUNCTION: Placental hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin
CC receptor expression in the endometrium. This results in the

suppression of the pulsatile endometrial release of the luteolytic hormone prostaglandin F2-alpha, hindering the regression of the corpus luteum (luteolysis) and therefore a return to ovarian cyclicity. This, and a possible direct effect of IFN-tau on prostaglandin synthesis, leads in turn to continued ovarian progesterone secretion, which stimulates the secretion by the endometrium of the nutrients required for the growth of the conceptus. In summary, displays particularly high antiviral and antiproliferative potency concurrently with particular weak cytotoxicity, high antiluteolytic activity and immunomodulatory properties. In contrast with other IFNs, IFN-tau is not virally inducible.

CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.

CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in the mononuclear cells of the extra-embryonic trophoderm.

CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the sheep conceptus between days 13 and 21 of pregnancy.

CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from IFN-omega genes in the ruminantia suborder and have continued to duplicate independently in different lineages of the ruminantia. They encode for proteins very similar in sequence but with different biological potency and pattern of expression.

CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-alpha1 subfamily.

CC -----

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CC -----

DR EMBL: Y00287; CA68396.1; -.

DR PIR: S03799; J50204.

DR PDB: 1BSL; X-ray; @=24-195.

DR InterPro: IPR009079; 4_helix_cytokine.

DR InterPro: IPR000471; Interferon_abd.

DR Pfam: PF00143; Interferon: 1.

DR PRINTS: PR00266; INTERFERONAB.

DR ProDom: PD000550; Interferon_abd. 1.

DR PROSITE: PS00252; INTERFERON_A_B_D; 1.

KW 3D-structure; Antiviral; Cytokine; Hormone; Multigene family;

KW Pregnancy; Signal.

FT CHAIN 1 23 By similarity.

FT DISULFID 24 195 Interferon_tau-1.

FT DISULFID 24 122 By similarity.

FT DISULFID 52 162 By similarity.

FT TURN 25 26

FT HELIX 27 46

FT TURN 47 47

FT TURN 47 47

FT HELIX 63 63

FT TURN 64 68

FT TURN 69 69

FT HELIX 73 95

FT TURN 96 97

FT TURN 100 101

FT HELIX 103 122

FT HELIX 138 156

FT TURN 157 159

FT HELIX 161 186

SO SEQUENCE 195 AA; 22192 MW; A495AE25DEA5BC9 CRC64;

Query Match 100.0%; Score 907; DB 1; Length 195;

Best Local Similarity 100.0%; Pred. No. 3.3e-76;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKLLDNRNRLSPHSCQDRKDFGLPGEMVGGDLOKQAPVLYEM 60

DB 24 CYLSRKMLDARENKLLDNRNRLSPHSCQDRKDFGLPGEMVGGDLOKQAPVLYEM 83

QY 61 LQGSFNLFTYEHSSAAMDITLLBQLCTGLQOQLDHLDTGCGQVGEDESLGNMDPIVTV 120

DB 84 LQGSFNLFTYEHSSAAMDITLLBQLCTGLQOQLDHLDTGCGQVGEDESLGNMDPIVTV 143

QY 121 KKYFQGIYDYLQKGYSDCAWEIVYEMMALVSTTLQRLTKMGDLSNP 172

DB 144 KKYFQGIYDYLQKGYSDCAWEIVYEMMALVSTTLQRLTKMGDLSNP 195

RESULT 2

INT2 SHEEP STANDARD; PRT; 195 AA.

ID INT2_SHEEP

AC P56829; P08316;

DT 01-AUG-1988 (Rel. 08, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE 05-JUN-2004 (Rel. 44, Last annotation update)

DE Interferon tau-2 precursor (IFN-tau2) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).

GN Name=IFNT2;

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.

OC NCBI_TaxID=9940;

OX NCBI_TaxID=9940;

LN [1]

RP SEQUENCE FROM N.A. (IFN-TAU2C).

RX MEDLINE=90040431; PubMed=2530342;

RA Stewart H.J., Flint A.P., Lamming G.E., McCann S.H., Parkinson T.J.; "Antiluteolytic effects of blastocyst-secreted interferon investigated in vitro and in vivo in the sheep."; J. Reprod. Fert. 37:127-138 (1989).

LN [2]

RP SEQUENCE FROM N.A. (IFN-TAU2C).

RX MEDLINE=89351557; PubMed=2475129;

RA Stewart H.J., McCann S.H., Northrop A.J., Lamming G.E., Flint A.P.; "Sheep antiluteolytic interferon: cDNA sequence and analysis of mRNA levels."; J. Mol. Endocrinol. 2:65-70 (1989).

LN [3]

RP SEQUENCE FROM N.A. (IFN-TAU2C).

RC TISSUE=Embryo;

RX MEDLINE=89326151; PubMed=2753362; DOI=10.1016/0378-1119(89)90082-6;

RA Charlier M., Hue D., Marcal J., Gaye P.; "Cloning and expression of cDNA encoding ovine trophoblastin: its identity with a class-II alpha interferon."; Gene 77:341-346 (1989).

LN [4]

RP SEQUENCE FROM N.A. (IFN-TAU2C).

RX MEDLINE=91067497; PubMed=1701245;

RA Klemann S.W., Imakawa K., Roberts R.M.; "Sequence variability among ovine trophoblast interferon cDNA."; Nucleic Acids Res. 18:6724-6724 (1990).

LN [5]

RP SEQUENCE OF 24-195 FROM N.A. (IFN-TAU2A AND IFN-TAU2B).

RC TISSUE=Embryo;

RA Winkelman G.L., Roberts R.M., Peterson A.J., Alexenko A.P., Ealy A.D.; "Identification of the expressed forms of ovine interferon-tau in the peri-implantation conceptus: sequence relationships and comparative biological activities."; Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

LN [6]

RP SEQUENCE OF 24-68.

RX MEDLINE=88137579; PubMed=3254170; DOI=10.1016/0014-5793(88)80574-X;

RA Charigny G., Re naud P., Hue t J.-C., Guillomot M., Charlier M., Pernellet J.-C., Marcal J.; "High homology between a trophoblastic protein (trophoblastin) isolated from ovine embryo and alpha-interferons."; FEBS Lett. 228:12-16 (1988).

LN [7]

RP FUNCTION.

RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;

RA Spencer T.E., Bazer F.W.; "Ovine interferon tau suppresses transcription of the estrogen receptor and oxytocin receptor genes in the ovine endometrium."; Endocrinology 137:1144-1147 (1996).

[8]
 RP CIRCULAR DICHROISM ANALYSIS, AND 3D-STRUCTURE MODELING.
 RX MEDLINE=95062134; PubMed=791949;
 RA Jarpe M.A., Johnson H.M., Bazer F.W., Oct T.L., Curto E.V.,
 RA Krishna N.R., Pontzer C.H.;
 RT "Predicted structural motif of IFN tau.";
 RL Protein Eng. 7:863-867(1994).
 RN [9]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau."
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [10]
 RP REVIEW.
 RX MEDLINE=99081096; PubMed=9665498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Matcal J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinaud P.B.,
 RA Guillomot M.W., Charlier M.A., Charigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities.";
 RL Biochimie 80:755-777(1998).
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not vitally
 CC inducible.
 CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
 CC the mononuclear cells of the extra-embryonic trophoblast.
 CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
 CC sheep conceptus between days 13 and 21 of pregnancy.
 CC -1- POLYMORPHISM: There seems to be three variants of IFN-tau 2:
 CC A/P8V2/P7 (shown here), B/P8V4 and C/P8.
 CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
 CC IFN-omega genes in the ruminant suborder and have continued to
 CC duplicate independently in different lineages of the ruminantia.
 CC They encode for proteins very similar in sequence but with
 CC different biological potency and pattern of expression.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
 CC alpha1 subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL/ X07920; CAA30753.1; -;
 DR EMBL/ M26386; AAA31584.1; -;
 DR EMBL/ X56344; CAA39784.1; -;
 DR EMBL/ X56345; CAA39785.1; -;
 DR EMBL/ AF158818; AAD44970.1; -;
 DR EMBL/ AF158820; AAD44972.1; -;
 DR PIR/ S03799; JS0204.
 DR HSBP/ P56828; 185L.
 DR InterPro/ IPR009079; 4 helix cytokine.
 DR InterPro/ IPR000471; Interferon_abd.

DR Pfam, PF00143; Interferon: 1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR PRODOM; PD000550; Interferon abd. 1.
 DR PROSITE; PS00252; INTERFERON A B D; 1.
 KW Antiviral; Cytokine; Direct protein sequencing; Hormone;
 KW Multigene family; Polymorphism; Pregnancy; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 195 Interferon tau-2.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 FT VARIANT 106 106 E -> D (in IFN-tau2C).
 FT VARIANT 130 130 E -> K (in IFN-tau2B).
 SQ SEQUENCE 195 AA; 22192 MM; EC4DBE507C289C67 CMC64;
 Query Match 99.2%; Score 900; DB 1; Length 195;
 Best Local Similarity 98.8%; Pred. No. 1.5e-75;
 Matches 170; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CYLSRKMLDARENLKLDNRNRLSPHSCLODRDFFGLPQPMVWGDDLOKQDAFPVLYEM 60
 Db 24 CYLSQRLMLDARENLKLDNRNRLSPHSCLODRDFFGLPQPMVWGDDLOKQDAFPVLYEM 83
 Oy 61 LQSFNLFYTHSSAAMDITLLEQLCTGLQOQDLPTCRQGVNGEESLGNMPTVTV 120
 Db 84 LQSFNLFYTHSSAAMDITLLEQLCTGLQOQDLPTCRQGVNGEESLGNMPTVTV 143
 Oy 121 KKVFQGIYDYLOEKGYSDCAWEIVRVMRALIVSTTLQKRLTYMGDLSNP 172
 Db 144 KKVFQGIYDYLOEKGYSDCAWEIVRVMRALIVSTTLQKRLTYMGDLSNP 195
 RESULT 3
 INT3 SHEEP STANDARD; PRT; 172 AA.
 AC P56832;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-3 (IFN-tau3) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).
 GN Name=IFN3;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Winkelman G.L., Roberts R.M., Peterson A.J., Alexenko A.P., Baly A.D.;
 RT "Identification of the expressed forms of ovine interferon-tau in the
 RT peri-implantation conceptus: sequence relationships and comparative
 RT biological activities.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP FUNCTION.
 RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
 RA Spencer T.E., Bazer F.W.;
 RT "Ovine interferon tau suppresses transcription of the estrogen
 RT receptor and oxytocin receptor genes in the ovine endometrium.";
 RL Endocrinology 137:1144-1147(1996).
 RN [3]
 RP CIRCULAR DICHROISM ANALYSIS, AND 3D-STRUCTURE MODELING.
 RX MEDLINE=95062134; PubMed=791949;
 RA Jarpe M.A., Johnson H.M., Bazer F.W., Oct T.L., Curto E.V.,
 RA Krishna N.R., Pontzer C.H.;
 RT "Predicted structural motif of IFN tau.";
 RL Protein Eng. 7:863-867(1994).
 RN [4]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau.";

RL J. Interferon Cytokine Res. 15:1053-1060(1995).

RN [5]

RP REVIEW

RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;

RA Martal J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinard P.B.,

RA Guillotot M.W., Charpigny S.Y.;

RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-

RT ubiquitous expression, structure-function relationships, a pregnancy

RT hormonal embryonic signal and cross-species therapeutic

RT potentialities";

RL Biochimie 80:755-777(1998).

CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal

CC recognition of pregnancy. Interacts with endometrial receptors,

CC probably type I interferon receptors, and blocks estrogen receptor

CC expression, preventing the estrogen-induced increase in oxytocin

CC receptor expression in the endometrium. This results in the

CC suppression of the pulsatile endometrial release of the luteolytic

CC hormone prostaglandin F2-alpha, hindering the regression of the

CC corpus luteum (luteolysis) and therefore a return to ovarian

CC cyclicity. This, and a possible direct effect of IFN-tau on

CC prostaglandin synthesis, leads in turn to continued ovarian

CC progesterone secretion, which stimulates the secretion by the

CC endometrium of the nutrients required for the growth of the

CC conceptus. In summary, displays particularly high antiviral and

CC antiproliferative potency concurrently with particularly weak

CC cytotoxicity, high antiluteolytic activity and immunomodulatory

CC properties. In contrast with other IFNs, IFN-tau is not vitally

CC inducible.

CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.

CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in

CC the mononuclear cells of the extra-embryonic trophoblast.

CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the

CC sheep conceptus between days 13 and 21 of pregnancy.

CC -1- POLYMORPHISM: There seems to be two variants of IFN-tau 3: A/P8VI

CC (shown here) and B/P8V3.

CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from

CC IFN-omega genes in the ruminantia suborder and have continued to

CC duplicate independently in different lineages of the ruminantia.

CC They encode for proteins very similar in sequence but with

CC different biological potency and pattern of expression.

CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-

CC alpha1 subfamily.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: AF158817; AAD4969.1; -

DR EMBL: AF158819; AAD4971.1; -

DR HSSP: P56828; 1BSL.

DR InterPro: IPR003079; 4_helix_cytokine.

DR InterPro: IPR000471; Interferon_abd.

DR Pfam: PF00143; Interferon_1.

DR PRINTS: PR00266; INTERFERONAB.

DR PRODOM: PD000550; Interferon_abd.1.

DR PROSITE: PS00252; INTERFERON_A_B_D; FALSE NEG.

KW Antiviral; Cytokine; Hormone; Multigene family; Polymorphism;

KW Pregnancy.

FT DISULFID 1 99 By similarity.

FT DISULFID 29 139 T->S (in isoform B).

FT VARIANT 87 87 FE->S (in isoform B).

FT VARIANT 124 125 L->Y (in isoform B).

FT VARIANT 130 130 L->Y (in isoform B).

SQ SEQUENCE 172 AA; 19866 MW; 7BFF1F036545C8B2 CRC64;

Query March 97.9%; Score 888; DB 1; Length 172;

Best Local Similarity 97.7%; Pred. No. 1.6e-74;

Matches 168; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYLSRKLMDPARENKLLDMNRLSPHSCLODRKDFGLPOEMWEGDLOKDOAFPLVYEM 60

DB 1 CYLSERLMDARENKLLDMNRLSPHSCLODRKDFGLPOEMWEGDLOKDOAFPLVYEM 60

QY 61 LOOSFNLFTYEHSSAAMDITLLQLCTGLQOOLDHLDTCGQVWGEEDSELGNMDPIVTV 120

DB 61 LOOSFNLFTYEHSSAAMDITLLQLCTGLQOOLDHLDTCGQVWGEEDSELGNMDPIVTV 120

QY 121 KKYFGGYDYDLOKGYSDCAMEIVRWEMRALVSTTLQKRLTKMGSDLNSP 172

DB 121 KKYFGGYDYDLOKGYSDCAMEIVRWEMRALVSTTLQKRLTKMGSDLNSP 172

RESULT 4

INT4_SHEEP

ID INT4_SHEEP STANDARD; PRT; 195 AA.

AC Q28594;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Interferon tau-4 precursor (IFN-tau4) (Trophoblast protein-1) (TP-1)

DE (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein)

DE (P3).

GN Name=IFNT4;

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=91067497; PubMed=1701245;

RA Klemann S.W., Imakawa K., Roberts R.M.;

RT "Sequence variability among ovine trophoblast interferon cDNA.";

RL Nucleic Acids Res. 18:6724-6724(1990).

RN [2]

RP FUNCTION.

RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;

RA Spencer T.E., Bazer F.W.;

RT "Ovine Interferon tau suppresses transcription of the estrogen

RT receptor and oxytocin receptor genes in the ovine endometrium.";

RL Endocrinology 137:1144-1147(1996).

RN [3]

RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.

RX MEDLINE=95062134; PubMed=7971949;

RA Urpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curro E.V.,

RA Krishna N.R., Pontzer C.H.;

RT "Predicted structural motif of IFN tau.";

RL Protein Eng. 7:863-867(1994).

RN [4]

RP 3D-STRUCTURE MODELING.

RX MEDLINE=96318252; PubMed=8746786;

RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;

RT "A three-dimensional model of interferon-tau.";

RL J. Interferon Cytokine Res. 15:1053-1060(1995).

RN [5]

RP REVIEW

RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;

RA Martal J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinard P.B.,

RA Guillotot M.W., Charpigny S.Y.;

RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-

RT ubiquitous expression, structure-function relationships, a pregnancy

RT hormonal embryonic signal and cross-species therapeutic

RT potentialities";

RL Biochimie 80:755-777(1998).

CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal

CC recognition of pregnancy. Interacts with endometrial receptors,

CC probably type I interferon receptors, and blocks estrogen receptor

CC expression, preventing the estrogen-induced increase in oxytocin

CC receptor expression in the endometrium. This results in the

CC suppression of the pulsatile endometrial release of the luteolytic

CC hormone prostaglandin F2-alpha, hindering the regression of the

corpus luteum (luteolysis) and therefore a return to ovarian cyclicity. This, and a possible direct effect of IFN-tau on prostaglandin synthase, leads in turn to continued ovarian progesterone secretion, which stimulates the secretion by the endometrium of the nutrients required for the growth of the conceptus. In summary, displays particularly high antiviral and antiproliferative potency concurrently with particular weak cytotoxicity, high antiluteolytic activity and immunomodulatory properties. In contrast with other IFNs, IFN-tau is not vitally inducible.

-1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.

-1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in the mononuclear cells of the extra-embryonic trophoctoderm.

-1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the sheep conceptus between days 13 and 21 of pregnancy.

-1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from IFN-omega genes in the ruminantia suborder and have continued to duplicate independently in different lineages of the ruminantia. They encode for proteins very similar in sequence but with different biological potency and pattern of expression.

-1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-alpha11 subfamily.

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CC EMBL: X56341, CA93781.1; -.

DR HSBP; P56828; 185L.

DR InterPro; IPR009079; 4_helix_cytokine.

DR InterPro; IPR000471; Interferon_abd.

DR Pfam; PF00143; Interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR PRODOM; PD000550; Interferon_abd; 1.

DR PROSITE; PS00253; INTERFERON_A_B_D; 1.

DR Antiviral; Cytokine; Hormone; Multigene family; Pregnancy; Signal.

FT SIGNAL 1 23 By similarity.

FT CHAIN 24 195 Interferon tau-4.

FT DISULFID 24 122 By similarity.

FT DISULFID 52 162 By similarity.

SQ SEQUENCE 195 AA; 22209 MW; 408BD4BDF5AA931 CRC64;

Query Match 97.1%; Score 881; DB 1; Length 195;

Best Local Similarity 96.5%; Pred. No. 8.5e-74;

Matches 166; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYSLKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVEGDLQKQAPVLYEM 60

DB 24 CYSQRMLDLARENKLLDRNRLSPHSCLODRKDFGLPQEMVEGDLQKQAPVLYEM 83

QY 61 LQGSFNFYTHSSAANDTTLLEGLCTGLQOOLDLDTCRGQVNGEBSSEIGNDPIVTY 120

DB 84 LQGSFNFYTHSSAANDTTLLEGLCTGLQOOLDLDTCRGQVNGEBSSEIGNDPIVTY 143

QY 121 KKYVQGIYDVLOEKGYSDCAWEIVREVMRALVTTLQKRLTKGQGLNSP 172

DB 144 KKYVQGIHDIYLOEKGYSDCAWEIVREVMRALVTTLQKRLTKGQGLNSP 195

RESULT 5

INT7 SHEEP STANDARD; PRT; 195 AA.

AC 008071;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Interferon tau-7 precursor (IFN-tau7) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein) (TP-07).

GN Name=IFNT7;

OS Ovis aries (sheep).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metazoa; Chordata; Euteleostomi; Euteleostomi;

OC Caprinae; Ovis.

OC NCBI_Taxid=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=trophoctoderm;

RX MEDLINE=93250155; PubMed=9485241;

RA Nephew K.P., Whaley A.E., Christenson R.K., Imakawa K.;

RT "Differential expression of distinct mRNAs for ovine trophoblast protein-1 and related sheep type I interferons."

RL Biol. Reprod. 48:768-778 (1993).

RL [2]

RP FUNCTION.

RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;

RA Spencer T.E., Bazer F.W.;

RT "Ovine interferon tau suppresses transcription of the estrogen receptor and oxytocin receptor genes in the ovine endometrium."

RL Endocrinology 137:1144-1147 (1996).

RL [3]

RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.

RX MEDLINE=95062134; PubMed=7971949;

RA Jarpe M.A., Johnson H.M., Bazer F.W., Oct T.L., Curto E.V.,

RA Krishna N.R., Pontzer C.H.;

RT "Predicted structural motif of IFN tau."

RL Protein Eng. 7:863-867 (1994).

RL [4]

RP 3D-STRUCTURE MODELING.

RX MEDLINE=96318252; PubMed=746786;

RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;

RT "A three-dimensional model of interferon-tau."

RL J. Interferon Cytokine Res. 15:1053-1060 (1995).

RL [5]

RP REVIEW.

RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;

RA Martal J.L., Chene N.M., Huynh L.P., L'Hartidon R.M., Renaud P.B.,

RA Guillouet M.W., Charlier M.A., Charpigny S.Y.;

RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-ubiquitous expression, structure-function relationships, a pregnancy hormonal embryonic signal and cross-species therapeutic potentialities."

RL Biochimie 80:755-777 (1998).

RL [1-]

RP FUNCTION: Parturition hormone primarily responsible for maternal recognition of pregnancy. Interacts with endometrial receptors, probably type I interferon receptors, and blocks estrogen receptor expression, preventing the estrogen-induced increase in oxytocin receptor expression in the endometrium. This results in the suppression of the pulsatile endometrial release of the luteolytic hormone prostaglandin F2-alpha, hindering the regression of the corpus luteum (luteolysis) and therefore a return to ovarian cyclicity. This, and a possible direct effect of IFN-tau on prostaglandin synthesis, leads in turn to continued ovarian progesterone secretion, which stimulates the secretion by the endometrium of the nutrients required for the growth of the conceptus. In summary, displays particularly high antiviral and antiproliferative potency concurrently with particular weak cytotoxicity, high antiluteolytic activity and immunomodulatory properties. In contrast with other IFNs, IFN-tau is not vitally inducible.

-1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.

-1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in the mononuclear cells of the extra-embryonic trophoctoderm.

-1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the sheep conceptus between days 13 and 21 of pregnancy.

-1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from IFN-omega genes in the ruminantia suborder and have continued to duplicate independently in different lineages of the ruminantia. They encode for proteins very similar in sequence but with different biological potency and pattern of expression.

-1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-alpha11 subfamily.

```

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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: M88771, AAA31505.1, -.
DR PIR: I47068, I47068.
DR HSPB: P56828, IBSL.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd_1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR Antiviral: Cytokine; Hormone; Multigene family; Pregnancy; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 195 Interferon tau-7.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
SQ SEQUENCE 195 AA; 22223 MW; 144ADE80A8B48 CRC64;

Query Match 97.0%; Score 880; DB 1; Length 195;
Best Local Similarity 96.5%; Pred. No. 1,1e-73;
Matches 166; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYLSKMLDARENLKLLDRNRSLPSHSCLODRDFGLPQEMVEGDLQKQAFVLYEM 60
DB 24 CYLSRRMLDARENLKLLDRNRSLPSHSCLODRDFGLPQEMVEGDLQKQAFVLYEM 83
QY 61 LQSFNLPYTHSSAAMDITLLEQLCTGLQQLPHLPTRCGQVWGESELSGNMDPIVTV 120
DB 84 LQSFNLPYTHSSAAMDITLLEQLCTGLQQLPHLPTRCGQVWGESELSGNMDPIVTV 143
QY 121 KKVFQGIYDYLQENKYSDCAMEIVVEMMRALTVSTTLQKRLTTCGDLNSP 172
DB 144 KKVFQGIYDYLQENKYSDCAMEIVVEMMRALTVSTTLQKRLTTCGDLNSP 195

RESULT 6
INTS SHEEP STANDARD; PRT; 195 AA.
AC 028595;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau-5 precursor (IFN-taus) (Trophoblast protein-1)
DE (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein)
DE (P5).
GN Name:IFNT5;
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCB1_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91067497; PubMed=1701245;
RA Klemann S.W., Inakawa K., Roberts R.M.;
RT "Sequence variability among ovine trophoblast interferon cDNA.";
RL Nucleic Acids Res. 18:6724-6724(1990).
RN [2]
RP FUNCTION.
RX MEDLINE=66174804; PubMed=6603586; DOI=10.1210/en.137.3.1144;
RA Spencer T.E., Bazer F.W.;
RT "Ovine interferon tau suppresses transcription of the estrogen
RT receptor and oxytocin receptor genes in the ovine endometrium.";
RL Endocrinology 137:1144-1147(1996).
RN [3]
RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.

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RX MEDLINE=95062134; PubMed=7971949;
RA Jarpe M.A., Johnson H.M., Bazer F.W., Oct T.L., Curro E.V.,
RA Kishna N.R., Pontzer C.H.;
RT "Predicted structural motif of IFN tau.";
RL Protein Eng. 7:863-867(1994).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96318252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau.";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [5]
RP REVIEW.
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Merial J.L., Chene N.M., Huynh L.P., L'Hardion R.M., Re naud P.B.,
RA Guillomot M.W., Charlier M.A., Chapigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT hormonal embryonic signal and cross-species therapeutic
RT potentialities.";
RL Biochimie 80:755-777(1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin
CC receptor expression in the endometrium. This results in the
CC suppression of the pulsatile endometrial release of the luteolytic
CC hormone prostaglandin F2-alpha, hindering the regression of the
CC corpus luteum (luteolysis) and therefore a return to ovarian
CC cyclicity. This, and a possible direct effect of IFN-tau on
CC prostaglandin synthesis, leads in turn to continued ovarian
CC progesterone secretion, which stimulates the secretion by the
CC endometrium of the nutrients required for the growth of the
CC conceptus. In summary, displays particularly high antiviral and
CC antiproliferative potency concurrently with particular weak
CC cytotoxicity, high antiluteolytic activity and immunomodulatory
CC properties. In contrast with other IFNs, IFN-tau is not virally
CC inducible.
CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
CC the mononuclear cells of the extra-embryonic trophoblast.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC sheep conceptus between days 13 and 21 of pregnancy.
CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alphaII subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announce/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: X63342; CA33782.1, -.
DR HSPB: P56828, IBSL.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd_1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR Antiviral: Cytokine; Hormone; Multigene family; Pregnancy; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 195 Interferon tau-5.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
SQ SEQUENCE 195 AA; 22163 MW; 14EA9038CB60A562 CRC64;

```


AC Q08072;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-8 precursor (IFN-tau8) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein)
 DE (TP-08).
 GN Name=IFNT8;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Trophoderm;
 RX MEDLINE=93250155; PubMed=8485241;
 RA Nephew K.P., Whaley A.E., Christenson R.K., Imakawa K.;
 RT "Differential expression of distinct mRNAs for ovine trophoblast
 RT protein-1 and related sheep type I interferons.";
 RL Biol. Reprod. 48:768-778(1993).
 RL [2]
 RP FUNCTION.
 RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
 RA Spencer T.E., Bazer F.W.;
 RT "Ovine interferon tau suppresses transcription of the estrogen
 RT receptor and oxytocin receptor genes in the ovine endometrium.";
 RL Endocrinology 137:1144-1147(1996).
 RN [3]
 RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
 RX MEDLINE=95062134; PubMed=7971949;
 RA Jape M.A., Johnson H.M., Bazer F.W., Ott T.L., Curto E.V.,
 RA Krishna N.R., Pontzer C.H.;
 RT "Predicted structural motif of IFN tau.";
 RL Protein Eng. 7:863-867(1994).
 RL [4]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitani Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau.";
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [5]
 RP REVIEW.
 RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Martell J.L., Chene N.M., Huynh L.P., L'Hardion R.M., Reinand P.B.,
 RA Gilmour M.W., Charlier M.A., Charigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities.";
 RL Biochimie 80:755-777(1998).
 CC -I- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not virally
 CC inducible.
 CC -I- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -I- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
 CC the mononuclear cells of the extra-embryonic trophoderm.
 CC -I- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
 CC sheep conceptus between days 13 and 21 of pregnancy.

CC -I- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
 CC IFN-omega genes in the ruminantia suborder and have continued to
 CC duplicate independently in different lineages of the ruminantia.
 CC They encode for proteins very similar in sequence but with
 CC different biological potency and pattern of expression.
 CC -I- SIMILARITY: Belongs to the alpha/beta interferon family, IFN-
 CC alpha1 subfamily.
 CC -----
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 CC -----
 CC EMBL; M88772; AAA31506.1; -;
 DR PIR; I47069; I47069.
 DR HSP; P56828; IBSL.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon_1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd; 1.
 DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
 KM Activiral; Cytokine; Hormone; Multigene family; Pregnancy; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 195 Interferon tau-8.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 SQ SEQUENCE 195 AA; 22157 MW; 7F92C56EC8DB5A8 CRC64;
 Query Match 95.4%; Score 865; DB 1; Length 195;
 Best Local Similarity 94.8%; Pred. No. 2.6e-72; Indels 0; Gaps 0;
 Matches 163; Conservative 6; Mismatches 3;
 QY 1 CYLSRKLMIDARENLKULDRMRLSPHSCQDRKDFGLPQEMVGGDLOKQDAFVLYEM 60
 DB 24 CYSQRMIDARENLRLDMRNLSPHSCQDRKDFGLPQEMVGGDLOKQDAFVLYEM 83
 QY 61 LQGSFNLFTYEHSSAANDTLLLEOLCTGLQOQLDHLDTGCGQVGEEDSELGNMDFIVTV 120
 DB 84 LQGSFNLFTYEHSSAANDTLLLEOLCTGLQOQLDHLDTGCGQVGEEDSELGNMDFIVTV 143
 QY 121 KKKFQGYDYLOKGYSDCAWEIVRVEEMRALFTVSTTLQKRLFTMGGLNSP 172
 DB 144 KKTFGIYDYLOKGYSDCAWEIVRVEEMRALFTVSTTLQKRLFTMGGLNSP 195
 RESULT 9
 INT_CAPHI
 ID INT_CAPHI STANDARD; PRT; 195 AA.
 AC P28171;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).
 GN Name=IFNT; Synonyms=CIP-1;
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Capra.
 OC NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92242937; PubMed=1374107;
 RA Leaman D.W., Roberts R.M.;
 RT "Genes for the trophoblast interferons in sheep, goat, and musk ox and
 RT distribution of related genes among mammals.";
 RL J. Interferon Res. 12:1-11(1992).
 RN [2]
 RP REVIEW.

RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Matcal J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinand P.B.,
 RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities".
 RL Biochimie 80:755-777(1998).
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not virally
 CC inducible.
 CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
 CC the mononuclear cells of the extra-embryonic trophoctoderm.
 CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
 CC conceptus during a very short period in early pregnancy.
 CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
 CC IFN-omega genes in the ruminant suborder and have continued to
 CC duplicate independently in different lineages of the ruminantia.
 CC They encode for proteins very similar in sequence but with
 CC different biological potency and pattern of expression.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
 CC alpha1 subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M73243; AAA30907.1; -;
 CC PIR: I46272; I46272.
 CC HSSP: P56828; 185L.
 CC InterPro: IPR009079; 4_helix_cytokine.
 CC InterPro: IPR000471; Interferon_abd.
 CC Pfam: PF00143; Interferon_1.
 CC PRINTS: PR00266; INTERFERONAB.
 CC PRODOM: PD000550; Interferon abd. 1.
 CC PROSITE: PS00252; INTERFERON_A_B_D, 1.
 CC Antiviral; Cytokine; Hormone; Pregnancy; Signal.
 CC SIGNAL 1 23 By similarity.
 CC CHAIN 24 195 Interferon tau.
 CC DISULFID 24 122 By similarity.
 CC DISULFID 52 162 By similarity.
 CC SEQUENCE 195 AA; 22172 MW; 049F91D3EB1CDB67 CRC64;
 SQ
 Query Match 93.3%; Score 846; DB 1; Length 195;
 Best Local Similarity 93.6%; Pred. No. 1.5e-70;
 Matches 161; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 Oy 1 CYLSRKMLDARENKILDRNRLSPHSCGLDRDRCFLGPMVWGCDQKQKAPVLYEM 60
 Db 24 CILSRRLMLDARENRLDRNRRLSPHSCGQDRDRCFLGPMVWGCDQKQKQASCVLVEM 83
 Oy 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLDHLDTDCRCQWGESELSGNMPTIVT 120
 Db 84 LQGSFNLFTYTHSSAAMDITLLDQCTGLDHLDTDCRCQWGESELSGNMPTIVT 143

Oy 121 KKYFOGIYDIYOEKGYSDCAMEIVREMMRALVTTLQKRLTMGGDLNSP 172
 Db 144 KKYFOGIYDIYOEKGYSDCAMEIVREMMRALVTTLQKRLTMGGDLNSP 195
 RESULT 10
 ID INT6 SHEEP STANDARD; PRT; 195 AA.
 AC Q29429;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-6 precursor (IFN-tau6) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).
 GN Name=IFNt6;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A. (IFN-TAU6D).
 RC TISSUE=Embryo;
 RX MEDLINE=91067497; PubMed=1701245;
 RA Klemann S.W., Imakawa K., Roberts R.M.;
 RT "Sequence variability among ovine trophoblast interferon cDNA.";
 RL Nucleic Acids Res. 18:6724-6724(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (IFN-TAU6D).
 RA Roberts R.M.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 24-195 FROM N.A. (IFN-TAU6A, IFN-TAU6B AND IFN-TAU6C).
 RC TISSUE=Embryo;
 RA Winkelman G.L., Roberts R.M., Peterson A.J., Alexenko A.P., Ealy A.D.;
 RT "Identification of the expressed forms of ovine interferon-tau in the
 RT peri-implantation conceptus: sequence relationships and comparative
 RT biological activities.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RA MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
 RA Spencer T.E., Bazer F.W.;
 RT "Ovine interferon tau suppresses transcription of the estrogen
 RT receptor and oxytocin receptor genes in the ovine endometrium.";
 RL Endocrinology 137:1144-1147(1996).
 RN [5]
 RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
 RX MEDLINE=95062134; PubMed=7971949;
 RA Jarpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curto E.V.,
 RA Krishna N.R., Pontzer C.H.;
 RT "Predicted structural motif of IFN tau.";
 RL Protein Eng. 7:863-867(1994).
 RN [6]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau.";
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [7]
 RP REVIEW.
 RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Matcal J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinand P.B.,
 RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities".
 RL Biochimie 80:755-777(1998).
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor

RA Ealy A.D., Wagner S.K., Sheila A.E., Whitley N.C., Klesling D.O.,
RA Barbaco G.F.,
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL: AY357338; AAC65197.1; -.
DR EMBL: AY357327; AAC65196.1; -.
DR HSSP: P56828; 1BSL.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-classes (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR00471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 22313 MW; C99AC236A716F654 CRC64;

Query March 91.5%; Score 830; DB 2; Length 195;
Best Local Similarity 92.4%; Pred. No. 4.7e-69;
Matches 159; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKILDRNRLSPHSCLODRKDFGLPQEMVEGDOIQKQAPVLYEM 60
DB 24 CYLSRRMLDARENILKILDRNRLSPHSCLODRKDFGLPQEMVEGDOIQKQAPVLYEM 83
QY 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQQOOLDLHLDTCRCQVNGEEDSEIGNMDPIVTV 120
DB 84 LQGFNLFYTHSSAAMDITLLLEQLCTGLQQOOLDLHLDTCRCQVNGEEDSEIGNMDPIVTV 143
QY 121 KKYFGIYDYLQEKYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
DB 144 KKYFGIYDYLQEKYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 195

RESULT 13
Q6RFZ8 PRELIMINARY; PRT; 172 AA.
AC Q6RFZ8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interferon tau (fragment).
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang X., Wang M., Xia C., Zhu D., Liou C., Bai Y.;
RL Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL: AY49657; AAR5892.1; -.
DR HSSP: P56828; 1BSL.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-classes (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR00471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT NON_TER 1
SQ SEQUENCE 172 AA; 19992 MW; 65984B2F91335046 CRC64;

Query March 90.0%; Score 816; DB 2; Length 172;
Best Local Similarity 91.3%; Pred. No. 8e-68;

Matches 157; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKILDRNRLSPHSCLODRKDFGLPQEMVEGDOIQKQAPVLYEM 60
DB 1 CYLSRRMLDARENILKILDRNRLSPHSCLODRKDFGLPQEMVEGDOIQKQAPVLYEM 60
QY 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQQOOLDLHLDTCRCQVNGEEDSEIGNMDPIVTV 120
DB 61 LQGFNLFYTHSSAAMDITLLLEQLCTGLQQOOLDLHLDTCRCQVNGEEDSEIGNMDPIVTV 120
QY 121 KKYFGIYDYLQEKYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
DB 121 KKYFGIYDYLQEKYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172

RESULT 14
INTA SHEEP STANDARD; PRT; 195 AA.
AC Q08053;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau-10 precursor (IFN-tau10) (Trophoblast protein-1) (TP-1)
DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein)
DE (TP-02).
GN Name=IFNT10;
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=trophoctodem;
RX MEDLINE=93250155; PubMed=8485241;
RA Nephew K.P., Whaley A.E., Christenson R.K., Imakawa K.;
RT "Differential expression of distinct mRNAs for ovine trophoblast
RT protein-1 and related sheep type I interferon.";
RL Biol. Reprod. 48:768-778 (1993).
RN [2]
RP FUNCTION.
RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
RA Spencer T.E., Bazer F.W.;
RT "Ovine interferon tau suppresses transcription of the estrogen
RT receptor and oxytocin receptor genes in the ovine endometrium.";
RL Endocrinology 137:1144-1147 (1996).
RN [3]
RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
RX MEDLINE=95062134; PubMed=7971949;
RA Jarpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curto E.V.,
RA Krishna N.R., Pontzer C.H.;
RT "Predicted structural motif of IFN tau.";
RL Protein Eng. 7:863-867 (1994).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96319252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau.";
RL J. Interferon Cytokine Res. 15:1053-1060 (1995).
RN [5]
RP REVIEW.
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.L., Chene N.M., Huynh L.P., L'Haxidon R.M., Reinaud P.B.,
RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT hormonal embryonic signal and cross-species therapeutic
RT potentialities.";
RL Biochimie 80:755-777 (1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin


```

DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-classes (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR Interferon; IPR009079; 4_helix_cytokine.
DR Interferon; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR Prodom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR Antiviral; Cytokine.
DR SEQUENCE 195 AA; 2236 MW; D37E646A8DE57FC4 CRC64;
SQ
Query Match 87.5%; Score 794; DB 2; Length 195;
Best Local Similarity 89.0%; Pred. No. 1e-65;
Matches 153; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CYSRKMLDARENLKLDNRNRLSPHSCLODRKDFGLPGEMVEGDQLQKQAFVLYEM 60
D 24 CYSRRMLDARENLKLDNRNRLSPHSCLODRKDFGLPGEMVEGDQLQKQAFVLYEM 83
Db 144 KRYFOGIDYLDQEKYSDCAMEIVRVMRALTSTTLQKRLTMGGDLNSP 195

Qy 61 LQGSFNLFTYEHSSAANDTLLBQLCTGLOQLDLDTCRGVNGEBSDELGNMPITV 120
D 84 LQGTFFNLFTYEHSSAANDTLLBQLCTGLOQLDLDTCRGLVNGEKSELGKMDPIMTV 143
Db 121 KRYFOGIDYLDQEKYSDCAMEIVRVMRALTSTTLQKRLTMGGDLNSP 172
D 144 KRYFOGIDYLDQEKYSDCAMEIVRVMRALTSTTLQKRLTMGGDLNSP 195

RESULT 17
06U242
ID 06U242 PRELIMINARY; PRT; 195 AA.
AC 06U242;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Interferon-tau 6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OC NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Ealy A.D., Wagner S.K., Sheila A.E., Whitley N.C., Klesling D.O.,
RA Barbato G.F.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; AY357336; AA056205.1; -.
DR HSSP; P56828; 1B5L.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005126; F:hematopoietin/interferon-classes (D200-domain. . .; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR Interferon; IPR009079; 4_helix_cytokine.
DR Interferon; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR Prodom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine.
DR SEQUENCE 195 AA; 2236 MW; FEE9F24431D41466 CRC64;
SQ
Query Match 86.7%; Score 786; DB 2; Length 195;
Best Local Similarity 89.0%; Pred. No. 5.7e-65;
Matches 153; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CYSRKMLDARENLKLDNRNRLSPHSCLODRKDFGLPGEMVEGDQLQKQAFVLYEM 60
D 24 CYSRRMLDARENLKLDNRNRLSPHSCLODRKDFGLPGEMVEGDQLQKQAFVLYEM 83
Qy 61 LQGSFNLFTYEHSSAANDTLLBQLCTGLOQLDLDTCRGVNGEBSDELGNMPITV 120

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Db 84 LQGTFFNLFTYEHSSAANDTLLBQLCTGLOQLDLDTCRGLVNGEKSELGKMDPIMTV 143
Qy 121 KRYFOGIDYLDQEKYSDCAMEIVRVMRALTSTTLQKRLTMGGDLNSP 172
Db 144 KRYFOGIDYLDQEKYSDCAMEIVRVMRALTSTTLQKRLTMGGDLNSP 195

RESULT 18
INT_OVIMO
ID INT_OVIMO STANDARD; PRT; 195 AA.
AC P28172;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
DE (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein).
GN Name=IFNT; Synonyms=IFN;
OS Ovis bos moschatus (Musko).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=31176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92242937; PubMed=1374107;
RA Leaman D.W., Roberts R.M.;
RT "Genes for the trophoblast interferons in sheep, goat, and musk ox and
RT distribution of related genes among mammals.";
RL J. Interferon Res. 12:1-11(1992).
RN [2]
RP REVIEW
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.L., Chene N.M., Huynh L.P., L'Hartidon R.M., Renaud P.B.,
RA Guillemot M.W., Charlier M.A., Charpigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT hormonal embryonic signal and cross-species therapeutic
RT potentialities.";
RL Biochimie 80:755-777(1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin
CC receptor expression in the endometrium. This results in the
CC suppression of the pulsatile endometrial release of the luteolytic
CC hormone prostaglandin F2-alpha, hindering the regression of the
CC corpus luteum (luteolysis) and therefore a return to ovarian
CC cyclicity. This, and a possible direct effect of IFN-tau on
CC prostaglandin synthesis, leads in turn to continued ovarian
CC progesterone secretion, which stimulates the secretion by the
CC endometrium of the nutrients required for the growth of the
CC conceptus. In summary, displays particularly high antiviral and
CC antiproliferative potency concurrently with particular weak
CC cytotoxicity, high antiluteolytic activity and immunomodulatory
CC properties. In contrast with other IFNs, IFN-tau is not virally
CC inducible.
CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
CC the mononuclear cells of the extra-embryonic trophoctoderm.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC conceptus during a very short period in early pregnancy.
CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alpha1i subfamily.
CC -----
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CC use by non-profit institutions as long as its content is in no way

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CC -----

DR EMBL; M73244; AAA31583.1; -.

DR HSSP; P56828; 185L.

DR InterPro; IPR009079; 4_helix_cytokine.

DR InterPro; IPR00471; Interferon_abd.

DR Pfam; PF00143; Interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR PRODOM; PD000550; Interferon_abd; 1.

DR PROSITE; PS00252; INTERFERON_A_B_D; 1.

DR Activital; Cytokine; Glycoprotein; Hormone; Pregnancy; Signal.

FT SIGNAL 1 23 By similarity.

FT CHAIN 24 195 Interferon_tau.

FT DISULFID 24 122 By similarity.

FT DISULFID 52 162 By similarity.

FT CARBOHYD 101 101 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 195 AA; 22370 MW; 39599512P3C34208 CRC64;

Query March 86.0%; Score 780; DB 1; Length 195;
Best Local Similarity 87.2%; Pred. No. 2.1e-64;
Matches 150; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKLDNRNRLSPHSCLDQRKDFGLPDMVWBGDLQKQDAFPVLYEM 60
DB 24 CYLSRRRPTLDVRENLRLLDRNRNRLSPHSCQDRKDFGLPDMVWBGDLQKQDALSVLYEM 83
QY 61 LQGSFNFPTFTHSSAANDTTLLEGLCTGLQOQLDHLDTCKGQVGEEDSEIGMMDPIVTV 120
DB 84 LQGFNFPTFTHSSCAANNNTTLLEGLRTGLHQLEDLDTCKGQVGEEDSEIGKMDPIVTV 143
QY 121 KKTFFQGIYDYLQEKGYSDCAMEIYRVEMMRALTIVSTTLQKRLTMGGDLNSP 172
DB 144 KKTFFQGIYDYLQEKGYSDCAMEIYRVEMMRALTIVSTTLQKRLTMGGDLNSP 195

RESULT 19
INTB SHEEP
ID INTB SHEEP STANDARD; PRT; 195 AA.
AC P28169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau-11 precursor (IFN-tau11) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antilituteolysin) (Trophoblast antilituteolytic protein) (p4) (S4).
GN Name=IFNT11;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92242937; Pubmed=1374107;
RA Leaman D.W., Roberts R.M.;
RT "Genes for the trophoblast interferons in sheep, goat, and musk ox and distribution of related genes among mammals.";
RT J. Interferon Res. 12:1-11(1992).
RN [2]
RP FUNCTION.
RX MEDLINE=66174804; Pubmed=8603586; DOI=10.1210/en.137.3.1144;
RA Spencer T.E., Bazer F.W.;
RT "Ovine interferon tau suppresses transcription of the estrogen receptor and oxytocin receptor genes in the ovine endometrium.";
RL Endocrinology 137:1144-1147(1996).
RN [3]
RP CIRCULAR DIGROISM ANALYSIS, AND 3D-STRUCTURE MODELING.
RX MEDLINE=95062134; Pubmed=7971949;
RA Jarpe M.A., Johnson H.M., Bazer F.W., Oct T.L., Curto E.V.,
RA Krishna N.R., Pontzer C.H.;
RT "Predicted structural motif of IFN tau.";

RL Protein Eng. 7:863-867(1994).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96318252; Pubmed=8746786;
RA Senda T., Saiton S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau.";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [5]
RP MUTAGENESIS.
RX MEDLINE=95014251; Pubmed=7929162;
RA Li J., Roberts R.M.;
RT "Structure-function relationships in the interferon-tau (IFN-tau). Changes in receptor binding and in antiviral and antiproliferative activities resulting from site-directed mutagenesis performed near the carboxyl terminus.";
RL J. Biol. Chem. 269:24826-24833(1994).
RN [6]
RP MUTAGENESIS.
RX MEDLINE=97156192; Pubmed=9002652;
RA Niswender K.D., Li J., Powell M.R., Loos K.R., Roberts R.M.,
RA Keister D.H., Smith M.F.;
RT "Effect of variants of interferon-tau with mutations near the carboxyl terminus on luteal life span in sheep.";
RL Biol. Reprod. 56:214-220(1997).
RN [7]
RP REVIEW.
RX MEDLINE=99081096; Pubmed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.L., Chene N.M., Huynh L.P., L'Hartidon R.M., Renaud P.B.,
RA Galliouc M.W., Charlier M.A., Charpigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-ubiquitous expression, structure-function relationships, a pregnancy hormonal embryonic signal and cross-species therapeutic potentialities.";
RL Biochimie 80:755-777(1998).
RN [8]
RP FUNCTION: Paracrine hormone primarily responsible for maternal recognition of pregnancy. Interacts with endometrial receptors, probably type I interferon receptors, and blocks estrogen receptor expression, preventing the estrogen-induced increase in oxytocin receptor expression in the endometrium. This results in the suppression of the pulsatile endometrial release of the luteolytic hormone prostaglandin F2-alpha, hindering the regression of the corpus luteum (luteolysis) and therefore a return to ovarian cyclicity. This, and a possible direct effect of IFN-tau on prostaglandin synthesis, leads in turn to continued ovarian progesterone secretion, which stimulates the secretion by the endometrium of the nutrients required for the growth of the conceptus. In summary, displays particularly high antiviral and antiproliferative potency concurrently with particular weak cytotoxicity, high antilituteolytic activity and immunomodulatory properties. In contrast with other IFNs, IFN-tau is not virally inducible.
RN [9]
RP SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in the mononuclear cells of the extra-embryonic trophoctoderm.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the sheep conceptus between days 13 and 21 of pregnancy.
CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from IFN-omega genes in the ruminantia suborder and have continued to duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-alpha1 subfamily.
CC
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EMBL; M73241; AAA31573.1; -.

DR PIR; 147097; 147097.
 DR HSBP; P01563; 2HE.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR009471; Interferon_abb.
 DR Pfam; PF00143; Interferon; 1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR PRODOM; PD000550; Interferon_abb; 1.
 DR PROSITE; PS00252; INTERFERON_AB_D; 1.
 DR Anticviral; Cytokine; Glycoprotein; Hormone; Multigene family;
 KW pregnancy; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 195 Interferon_tau-11.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 FT CARBOHYD 101 101 N-linked (GlcNAc...) (potential).
 FT MUTAGEN 166 166 I->T: 20-fold reduction in receptor binding activity, greatly reduced antiviral and almost abolished antiproliferative activity.
 FT MUTAGEN 183 183 Missing: Little effect on receptor binding activity but greatly reduced antiviral and almost abolished antiproliferative activity.
 FT MUTAGEN 183 183 Missing: Little effect on receptor binding activity but greatly reduced antiviral and almost abolished antiproliferative activity.
 FT MUTAGEN 185 195 Missing: Little effect on receptor binding activity but greatly reduced antiviral and almost abolished antiproliferative activity.
 FT SEQUENCE 195 AA; 22243 MW; DC6321E42BDF948A CRC64;
 SQ
 Query Match 85.8%; Score 778; DB 1; Length 195;
 Best Local Similarity 86.6%; Pred. No. 3, 2e-64;
 Matches 149; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENLKLDLRNRLSPHSCLDRKDFGLPOEWESEDOLOKQDAFFVLYEM 60
 24 CYLSGRMLDARENLRLDRNRRLSPHSCLDRKDFGLPOEWESEDOLOKQDAFFVLYEM 83
 Db 61 LQSGFNLFYTHSSAAMDPTLLLEQLCTGLQOQLDHLDTGRCQVGEEDSEIGNDPIVTV 120
 84 LQSGFNLFYTHSSAAMDPTLLLEQLCTGLQOQLDHLDTGRCQVGEEDSEIGNDPIVTV 143
 QY 121 KKYFGCIYDYLQEGYSCDCAWEIVVEMRALVTSTLOKRLTKYGGSLNSP 172
 144 KKYFGCIYDYLQEGYSCDCAWEIVVEMRALVTSTLOKRLTKYGGSLNSP 195
 Db
 RESULT 20
 INT1_BOVIN STANDARD; PRT; 195 AA.
 AC P15696; P15694; Q28126; Q28127; Q28128; Q28191; Q95NE2;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-1 precursor (IFN-tau) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antileucolysin) (Trophoblast antileucolytic protein).
 GN Name=IFN1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (IFN-TAU1A AND IFN-TAU1D).
 RX MEDLINE=89127268; PubMed=2521687;
 RA Imakawa K., Hansen T.R., Malachy P.-V., Anthony R.V., Polites H.G.,
 RA Marotai K.R., Roberts R.M.;
 RT "Molecular cloning and characterization of complementary
 RT deoxyribonucleic acids corresponding to bovine trophoblast protein-1:
 RT a comparison with ovine trophoblast protein-1 and bovine interferon-
 RT alpha II.";
 RL Mol. Endocrinol. 3:127-139(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (IFN-TAU1C).

RC TISSUE=Trophoblast;
 RX MEDLINE=90334707; PubMed=2378676;
 RA Stewart H.J., McCann S.H., Flint A.P.F.;
 RT "Structure of an interferon-alpha 2 gene expressed in the bovine
 RT conceptus early in gestation."
 RL J. Mol. Endocrinol. 4:275-282(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (IFN-TAU1A; IFN-TAU1B AND IFN-TAU1D).
 RX MEDLINE=91131606; PubMed=1704373;
 RA Hansen T.R., Leaman D.W., Cross J.C., Mathialagan N., Bixby J.A.,
 RA Roberts R.M.;
 RT "The genes for the trophoblast interferons and the related interferon-
 RT alpha II possess distinct 5'-promoter and 3'-flanking sequences";
 RL J. Biol. Chem. 266:3060-3067(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (IFN-TAU1C).
 RC TISSUE=Trophoblast;
 RA Stewart H.J.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (IFN-TAU1A).
 RA Roberts R.M.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (IFN-TAU1C).
 RA Chung Y.G., Seidel G.E. Jr.;
 RT "Cloning bovine interferon-tau genes and characterizing their
 RT transcriptional expression during early pregnancy";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 24-195 FROM N.A. (IFN-TAU1C).
 RA Larson S.F., Liu L., Winkelman G.L., Kubisch H.M., Bixby J.A.,
 RA Roberts R.M., Ealy A.D.;
 RT "The expressed genes for bovine interferon-tau: identification and
 RT expression during conceptus development."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau";
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [9]
 RP REVIEW.
 RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Martal J.L., Chene N.M., Huynh L.P., L'Haxidon R.M., Reinard P.B.,
 RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities";
 RL Biochimie 80:755-777(1998).
 CC -I- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antileucolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not vitally
 CC inducible.
 CC -I- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -I- TISSUE SPECIFICITY: Constitutively and extra-embryonic trophoblast.
 CC -I- DEVELOPMENTAL STAGE: Major secretory product synthesized by the

```

CC      bovine conceptus between days 15 and 25 of pregnancy.
CC      -1- POLYMORPHISM: There seems to be four variants of IFN-tau 1: A, B
CC      (shown here), C and D.
CC      -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC      IFN-omega genes in the ruminantia suborder and have continued to
CC      duplicate independently in different lineages of the ruminantia.
CC      They encode for proteins very similar in sequence but with
CC      different biological potency and pattern of expression.
CC      -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC      alpha11 subfamily.
CC      -----
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CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL; M31557; AAA50458.2; -
DR      EMBL; M31555; AAA50457.1; -
DR      EMBL; X65539; CAA46506.1; -
DR      EMBL; M60903; AAB67325.1; -
DR      EMBL; M60913; AAA62712.1; -
DR      EMBL; M60908; AAA62711.1; -
DR      EMBL; AF238612; AAG14169.1; -
DR      EMBL; AF196320; AAF08671.2; -
DR      PIR; A39505; A39505.
DR      PIR; B39505; B39505.
DR      PIR; S23751; S23751.
DR      HSP; P56828; IBSL.
DR      InterPro; IPR009079; 4 helix cytokine.
DR      InterPro; IPR000471; Interferon_abd.
DR      Pfam; PF00143; Interferon_1.
DR      PRINTS; PR00266; INTERFERONAB.
DR      PRODOM; PD000550; Interferon_abd.1.
DR      PROSITE; PS00252; INTERFERON_A_B_D_1.
KM      Antiviral; Cytokine; Glycoprotein; Hormone; Multigene family;
KM      Polymorphism; Pregnancy; Signal.
FT      SIGNAL      1      23      Probable.
FT      CHAIN      24      195      Interferon tau-1.
FT      DISULFID      24      122      By similarity.
FT      DISULFID      52      162      By similarity.
FT      CARBOHYD      101      101      N-linked (GlcNAc...) (Potential).
FT      VARIANT      29      29      D -> N (in IFN-tau1d).
FT      VARIANT      88      88      F -> L (in IFN-tau1A).
FT      VARIANT      169      169      V -> M (in IFN-tau1C and IFN-tau1D).
FT      CONFLICT      18      18      P -> Q (in Ref. 1; AAA50458).
FT      CONFLICT      20      20      R -> E (in Ref. 1; AAA50457).
SQ      SEQUENCE      195 AA; 22134 MW; FE98CFAS4AE86902 CRC64;
Query March      80.0%; Score 726; DB 1; Length 195;
Best Local Similarity      81.3%; Pred. No. 2.2e-59;
Matches 139; Conservative 13; Mismatches 19; Indels 0; Gaps 0;
QY      1      CYLSRKLMLDARENLKILDRNRLSPHSCLODRKDFGJPOBMVGGDLOKQDAFPVLYEM      60
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      24      CYLSSEDMGARENLRLRLARNRSLSPHPCLODRKDFGJPOBMVGGDLOKQDAISVLYHEM      83
QY      61      LQGSFNLFTYEHSSAANDTLLLEQLCTGLQOQLDHLDTCRGVNGEEDSELGNDPIVTV      120
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      84      LQQCFNLFYTEHSSAANNNTLLLEQLCTGLQOQLDHLDTCLGPNVNGEKSDMGKRGPIITLV      143
QY      121      KKYFGQIVYDLOEGKGYDCAEMEYRVEMRLALTYSTLQKRLTKMGDGLNS      171
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      144      KKYFGQIHVYLKEKESYDCAWEIIRVEMRLALSSSTLLQKRLRMGDGLNS      194

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DT      30-MAY-2000 (Ref. 39, last sequence update)
DT      05-JUN-2004 (Ref. 44, last annotation update)
DE      Interferon tau-2 (IFN-tau2) (trophoblast protein-1) (TP-1)
DE      (trophoblastin) (Antituteolytin) (trophoblast antituteolytic protein).
GN      Name=IFN2;
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=91308971; Pubmed=11416010; DOI=10.1210/en.142.7.2906;
RA      Ealy A.D., Larson S.F., Liu L., Alexenko A.P., Winkelman G.L.,
RA      Kubiach H.M., Bixdy U.A., Roberts R.M.;
RT      "Polymorphic forms of expressed bovine interferon-tau genes: relative
RT      transcript abundance during early placental development; promoter
RT      sequences of genes and biological activity of protein products.";
RL      Endocrinology 142:2906-2915(2001).
RN      [2]
RP      3D-STRUCTURE MODELING.
RX      MEDLINE=96318252; Pubmed=8746786;
RA      Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT      "A three-dimensional model of interferon-tau.";
RL      J. Interferon Cytokine Res. 15:1053-1060(1995).
RN      [3]
RP      REVIEW.
RX      MEDLINE=99081096; Pubmed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA      Martal J.L., Chene N.M., Huynh L.P., L'Havidon R.M., Reinard P.B.,
RA      Guillouet M.M., Charlier M.A., Charpigny S.Y.;
RT      "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT      ubiquitous expression, structure-function relationships, a pregnancy
RT      hormonal embryonic signal and cross-species therapeutic
RT      potentialities.";
RL      Biochimie 80:755-777(1998).
CC      -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC      recognition of pregnancy. Interacts with endometrial receptors,
CC      probably type I interferon receptors, and blocks estrogen receptor
CC      expression, preventing the estrogen-induced increase in oxytocin
CC      receptor expression in the endometrium. This results in the
CC      suppression of the pulsatile endometrial release of the luteolytic
CC      hormone prostaglandin F2-alpha, hindering the regression of the
CC      corpus luteum (luteolysis) and therefore a return to ovarian
CC      cyclicity. This, and a possible direct effect of IFN-tau on
CC      prostaglandin synthesis, leads in turn to continued ovarian
CC      progesterone secretion, which stimulates the secretion by the
CC      endometrium of the nutrients required for the growth of the
CC      conceptus. In summary, displays particularly high antiviral and
CC      antiproliferative potency concurrently with particular weak
CC      cytotoxicity, high antiluteolytic activity and immunomodulatory
CC      properties. In contrast with other IFNs, IFN-tau is not vitally
CC      inducible.
CC      -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC      -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
CC      the mononuclear cells of the extra-embryonic trophoderm.
CC      -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC      bovine conceptus between days 15 and 25 of pregnancy.
CC      -1- POLYMORPHISM: There seems to be three variants of IFN-tau 2: A
CC      (shown here), B and C.
CC      -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC      IFN-omega genes in the ruminantia suborder and have continued to
CC      duplicate independently in different lineages of the ruminantia.
CC      They encode for proteins very similar in sequence but with
CC      different biological potency and pattern of expression.
CC      -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC      alpha11 subfamily.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial

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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; AF196321; AAF08672.1; -
CC  DR  EMBL; AF196322; AAF08673.1; -
CC  DR  EMBL; AF196323; AAF08674.1; -
CC  DR  HSSP; P56828; 1B5L.
CC  DR  InterPro; IPR009079; 4_helix_cytokine.
CC  DR  InterPro; IPR000471; Interferon_abd.
CC  DR  Pfam; PF00143; Interferon_1.
CC  DR  PRINTS; PR00266; INTERFERONAB.
CC  DR  ProDom; PD000550; Interferon_abd; 1.
CC  DR  PROSITE; PS00252; INTERFERON_A_B_D; 1.
CC  KM  Antiviral; Cytokine; Glycoprotein; Hormone; Multigene family;
CC  Polymorphism; Pregnancy.
CC  FT  DISULFID 1 99 By similarity.
CC  FT  CARBOHYD 28 139 By similarity.
CC  FT  VARIANT 6 6 N-linked (GlcNAc... ) (Potential).
CC  FT  VARIANT 135 135 D -> N (in IFN-tau2B and IFN-tau2C).
CC  FT  VARIANT 146 146 E -> V (in IFN-tau2C).
CC  FT  VARIANT 146 146 M -> V (in IFN-tau2C).
CC  SQ  SEQUENCE 172 AA; 19892 MW; 30B19BE18540DE07 CRC64;

Query Match 79.5%; Score 721; DB 1; Length 172;
Best Local Similarity 80.7%; Pred. No. 5,4e-59;
Matches 138; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKILDRNRLSPHSCLQDRKDFGLPQEMVGECDLQKQAPFVLYEM 60
DB 1 CYLSEDHMLGARENRLRLARNRRLSPHPCLODRKDFGLPQEMVGECDLQKQAPFVLYEM 60
QY 61 LQGFNLFYTHSSAAMNTLLLEQCTGLQOQLEDLACLPVWGEKSDMGKRGPIITLV 120
DB 61 LQGFNLFYTHSSAAMNTLLLEQCTGLQOQLEDLACLPVWGEKSDMGKRGPIITLV 120
QY 121 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 171
DB 121 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 171
QY 121 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 171
DB 121 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 171

RESULT 22
Q8MJ29 PRELIMINARY; PRT; 172 AA.
AC Q8MJ29
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Interferon-tau1e (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN 11
RP KUDJesch H.M., Raemussen T.A., Johnson K.M.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; AF526881; AAM91995.1; -
DR HSSP; P56828; 1B5L.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005166; F:hematopoietin/interferon-c1aas (D200-domain...); IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR SMART; SM00076; IFabd; 1.
DR Antiviral; Cytokine.
FT NON TER 1 1
FT NON TER 172 172
SQ SEQUENCE 172 AA; 19815 MW; 220455164D20DF26 CRC64;

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Query Match 79.3%; Score 719; DB 2; Length 172;
Best Local Similarity 80.7%; Pred. No. 8.3e-59;
Matches 138; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKILDRNRLSPHSCLQDRKDFGLPQEMVGECDLQKQAPFVLYEM 60
DB 1 CYLSEDHMLGARENRLRLARNRRLSPHPCLODRKDFGLPQEMVGECDLQKQAPFVLYEM 60
QY 61 LQGFNLFYTHSSAAMNTLLLEQCTGLQOQLEDLACLPVWGEKSDMGKRGPIITLV 120
DB 61 LQGFNLFYTHSSAAMNTLLLEQCTGLQOQLEDLACLPVWGEKSDMGKRGPIITLV 120
QY 121 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 171
DB 121 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 171

RESULT 23
Q9MYK6 PRELIMINARY; PRT; 195 AA.
ID Q9MYK6
AC Q9MYK6
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Cow trophoblast protein-1 (TP-1).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN 11
RP SEQUENCE FROM N.A.
RL MEDLINE; 89127268; PubMed=2521687;
RX Imakawa K., Hansen T.R., Malachy P.V., Anthony R.V., Pojtees H.G.,
RA Maroteli K.R., Roberts R.M.;
RT "Molecular cloning and characterization of complementary
RT deoxyribonucleic acids corresponding to bovine trophoblast protein-1:
RT a comparison with ovine trophoblast protein-1 and bovine interferon-
RT alpha II."
RL Mol. Endocrinol. 3:127-139 (1989).
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; M31558; AAA50459.1; -
DR PIR; A40068; A40068.
DR HSSP; P56828; 1B5L.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005166; F:hematopoietin/interferon-c1aas (D200-domain...); IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KM Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 22201 MW; 42E16A2925FC41BB CRC64;

Query Match 79.1%; Score 717; DB 2; Length 195;
Best Local Similarity 79.5%; Pred. No. 1.5e-58;
Matches 136; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKILDRNRLSPHSCLQDRKDFGLPQEMVGECDLQKQAPFVLYEM 60
DB 1 CYLSEDHMLGARENRLRLARNRRLSPHPCLODRKDFGLPQEMVGECDLQKQAPFVLYEM 60
QY 24 CYLSEHMLGARENRLRLARNRRLSPHPCLODRKDFGLPQEMVGECDLQKQAPFVLYEM 83
DB 24 CYLSEHMLGARENRLRLARNRRLSPHPCLODRKDFGLPQEMVGECDLQKQAPFVLYEM 83
QY 61 LQGFNLFYTHSSAAMNTLLLEQCTGLQOQLEDLACLPVWGEKSDMGKRGPIITLV 120
DB 61 LQGFNLFYTHSSAAMNTLLLEQCTGLQOQLEDLACLPVWGEKSDMGKRGPIITLV 120
QY 84 LQGFNLFYTHSSAAMNTLLLEQCTGLQOQLEDLACLPVWGEKSDMGKRGPIITLV 143
DB 84 LQGFNLFYTHSSAAMNTLLLEQCTGLQOQLEDLACLPVWGEKSDMGKRGPIITLV 143
QY 121 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 171
DB 121 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 171
QY 144 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 194
DB 144 KKYFGIYDYLQEGYSDCAMEIYVEMRALTVSTLQKRLTKMGDGLNS 194

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RESULT 24
INT3_BOVIN STANDARD; PRT; 172 AA.
AC P56831; Q9M209;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau-3 (IFN-tau3) (Trophoblast protein-1) (TP-1)
DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).
GN Name=IFN3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
OX [1]
RP SEQUENCE FROM N.A. (IFN-TAU3A; IFN-TAU3B; IFN-TAU3C AND IFN-TAU3D).
RC TISSUE=Blasocyst; and Embryo;
RA Larson S.F., Liu L., Winkelman G.L., Kubisch H.M., Alexenko A.P.,
RA Bixby J.A., Roberts R.M., Baly A.D.;
RA "Polymorphisms among the expressed genes for bovine interferon-tau:
RT identification and expression during early placental development.";
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (IFN-TAU3E).
RC TISSUE=Blasocyst;
RA Larson S.F., Liu L., Winkelman G.L., Kubisch H.M., Alexenko A.P.,
RA Bixby J.A., Roberts R.M., Baly A.D.;
RA "Polymorphisms among the expressed genes for bovine interferon-tau:
RT identification and expression during early placental development.";
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP 3D-STRUCTURE MODELING.
RA MEDLINE=96318252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RA "A three-dimensional model of interferon-tau";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [4]
RP REVIEW.
RA MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Maccall J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinard P.B.,
RA Guillouet M.W., Charlier M.A., Chapigny S.Y.;
RA "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT hormonal embryonic signal and cross-species therapeutic
RT potentialities";
RL Biochimie 80:755-777(1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin
CC receptor expression in the endometrium. This results in the
CC suppression of the pulsatile endometrial release of the luteolytic
CC hormone prostaglandin F2-alpha, hindering the regression of the
CC corpus luteum (luteolysis) and therefore a return to ovarian
CC cyclicity. This, and a possible direct effect of IFN-tau on
CC prostaglandin synthesis, leads in turn to continued ovarian
CC progesterone secretion, which stimulates the secretion by the
CC endometrium of the nutrients required for the growth of the
CC conceptus. In summary, displays particularly high antiviral and
CC antiproliferative potency concurrently with particular weak
CC cytotoxicity, high antiluteolytic activity and immunomodulatory
CC properties. In contrast with other IFNs, IFN-tau is not vitally
CC inducible.
CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
CC the mononuclear cells of the extra-embryonic trophoblastoderm.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC bovine conceptus between days 15 and 25 of pregnancy.
CC -1- POLYMORPHISM: There seems to be five variants of IFN-tau 3: A
CC (shown here), B, C, D and E.

CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alpha1 subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AF196324; AAF08675.1; -;
DR EMBL; AF196325; AAF08676.1; -;
DR EMBL; AF196326; AAF08677.1; -;
DR EMBL; AF196327; AAF08678.1; -;
DR EMBL; AF270471; AAF74783.1; -;
DR HSSP; P56828; 1BSL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd.1.
DR PROSITE; PS00252; INTERFERON_A_B_D; FALSE_NEG.
KW Antiviral; Cytokine; Glycoprotein; Hormone; Multigene family;
KW Polymorphism; Pregnancy.
FT DISULFID 1 99 By similarity.
FT DISULFID 29 139 By similarity.
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT VARIAT 25 25 S -> P (in IFN-tau3D).
FT VARIAT 76 76 A -> S (in IFN-tau3B).
FT VARIAT 126 126 V -> G (in IFN-tau3E).
FT VARIAT 129 129 D -> A (in IFN-tau3C).
FT VARIAT 146 146 V -> M (in IFN-tau3E).
SQ SEQUENCE 172 AA; 19774 MW; B02F38A09C38863 CRC64;
Query Match 77.9%; Score 707; DB 1; Length 172;
Best Local Similarity 79.5%; Pred. No. 1,le-57;
Matches 136; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
QY 1 CYLSRKMLDARNTKILDMNRLSPHSCUDRKPGLPEQWVGDLQXQAPVLYEM 60
DB 1 CYLSEDMGLARENLRLARKNRLSPHPCQDRKDFELPEQWVGSQLQXQDAISLVHEM 60
QY 61 LQGSFNLFTYEHSSAAMDITLLEQLCTGLQOQLDHLDTCRGOVWGEEDSELGNMPTIVTV 120
DB 61 LQGSFNLFTYEHSSAAMDITLLEQLCTGLQOQLDHLDTCRGOVWGEEDSELGNMPTIVTV 120
QY 121 KKYFQGIYDYLDKQKSDSCAMEIVRWMPALVTSTTLQKRLTGMGDLNS 171
DB 121 KKYFQGIYDYLDKQKSDSCAMEIVRWMPALVTSTTLQKRLTGMGDLNS 171
DB 121 KKYFQGIYDYLDKQKSDSCAMEIVRWMPALVTSTTLQKRLTGMGDLNS 171
RESULT 25
Q9GLI6
ID Q9GLI6 PRELIMINARY; PRT; 195 AA.
AC Q9GLI6;
DT 01-MAR-2001 (TREMURel. 16, Created)
DT 01-MAR-2001 (TREMURel. 16, Last sequence update)
DT 01-MAR-2004 (TREMURel. 26, Last annotation update)
DE Interferon tau.
GN Name=IFN-tau-c3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
OX [1]
RP SEQUENCE FROM N.A.

RA Chung Y.G., Seidel G.E. Jr.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL: AF238611; AAG14168.1; -.
 DR PIR: A40068; A40068.
 DR HSP: P56828; IBSL.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005126; F:hematopoietin/interferon-c-las (D200-domain. . .; IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR000471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR ProDom: PD000550; Interferon_abd; 1.
 DR SMART: SM00076; IFabd; 1.
 DR Antiviral: Cytokine.
 KW SEQUENCE 195 AA; 22160 MW; 6DB1FAE39BF033FA CRC64;
 SQ
 Query Match 77.4%; Score 702; DB 2; Length 195;
 Best Local Similarity 78.9%; Pred. No. 3.7e-57;
 Matches 135; Conservative 13; Mismatches 23; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKLLDRMNRSLSPHSCLODRKDFGLPQEMVEGDDQLQKQDAFPVLYEM 60
 DB 24 CYLSEDMHLAGRENRLRLAQRNRLSPHSCLODRKDFGLPQEMVEGDDQLQKQDAISVLHEM 83
 QY 61 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVNGEBSDELGNDDPIVTV 120
 DB 84 LQGFNLFHIEHSSAAMNTTLLEQLCTGLQOQLDHLDTCRGQVNGEBSDELGNDDPIVTV 143
 QY 121 KKYFGIYDYLQEGYSDCAWEIYRVEMRALTSTTLQKRLTGMGGLNS 171
 DB 144 KKYFQIHVYLKKEYSDCAMEIIRVEMRALTSTTLQKRLTGMGGLNS 194
 RESULT 26
 Q6DUN3 PRELIMINARY; PRT; 172 AA.
 ID Q6DUN3
 AC Q6DUN3;
 DT 25-OCT-2004 (TREMblrel. 28; Created)
 DT 25-OCT-2004 (TREMblrel. 28; Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28; Last annotation update)
 DE Interferon tau2 (Fragment).
 OS Bison bison (American Bison).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bison.
 OX NCBI_TaxID=9901;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rasmussen T.A., Ealy A.D., Kubisch H.M.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL: AY643747; AAT67216.1; -.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005126; F:hematopoietin/interferon-c-las (D200-domain. . .; IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR000471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR ProDom: PD000550; Interferon_abd; 1.
 DR SMART: SM00076; IFabd; 1.
 DR Antiviral: Cytokine.
 FT NON_TER 1
 FT NON_TER 172
 SQ SEQUENCE 172 AA; 19764 MW; 7E41012B093889E1 CRC64;
 Query Match 76.7%; Score 696; DB 2; Length 172;
 Best Local Similarity 78.4%; Pred. No. 1.1e-56;
 Matches 134; Conservative 15; Mismatches 22; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKLLDRMNRSLSPHSCLODRKDFGLPQEMVEGDDQLQKQDAFPVLYEM 60

DB 1 CYLSEDMHLAGRENRLRLAQRNRLSPHSCLODRKDFGLPQEMVEGDDQLQKQDAISVLHEM 60
 QY 61 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVNGEBSDELGNDDPIVTV 120
 DB 61 LQGFNLFHIEHSSAAMNTTLLEQLCTGLQOQLDHLDTCRGQVNGEBSDELGNDDPIVTV 143
 QY 121 KKYFGIYDYLQEGYSDCAWEIYRVEMRALTSTTLQKRLTGMGGLNS 171
 DB 121 KKYFQIHVYLKKEYSDCAMEIIRVEMRALTSTTLQKRLTGMGGLNS 194
 RESULT 27
 Q9GLLS PRELIMINARY; PRT; 195 AA.
 ID Q9GLLS
 AC Q9GLLS;
 DT 01-MAR-2001 (TREMblrel. 16; Created)
 DT 01-MAR-2001 (TREMblrel. 16; Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26; Last annotation update)
 DE Interferon tau.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chung Y.G., Seidel G.E. Jr.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL: AF238613; AAG14170.1; -.
 DR HSP: P56828; IBSL.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005126; F:hematopoietin/interferon-c-las (D200-domain. . .; IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR000471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR ProDom: PD000550; Interferon_abd; 1.
 DR SMART: SM00076; IFabd; 1.
 DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
 KW Antiviral; Cytokine.
 KW SEQUENCE 195 AA; 22139 MW; 689C2443B203E50A CRC64;
 SQ
 Query Match 76.4%; Score 693; DB 2; Length 195;
 Best Local Similarity 78.4%; Pred. No. 2.5e-56;
 Matches 134; Conservative 15; Mismatches 22; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKLLDRMNRSLSPHSCLODRKDFGLPQEMVEGDDQLQKQDAFPVLYEM 60
 DB 24 CYLSEDMHLAGRENRLRLAQRNRLSPHSCLODRKDFGLPQEMVEGDDQLQKQDAISVLHEM 83
 QY 61 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVNGEBSDELGNDDPIVTV 120
 DB 84 LQGFNLFHIEHSSAAMNTTLLEQLCTGLQOQLDHLDTCRGQVNGEBSDELGNDDPIVTV 143
 QY 121 KKYFGIYDYLQEGYSDCAWEIYRVEMRALTSTTLQKRLTGMGGLNS 171
 DB 144 KKYFQIHVYLKKEYSDCAMEIIRVEMRALTSTTLQKRLTGMGGLNS 194
 RESULT 28
 INT_GIRCA STANDARD; PRT; 195 AA.
 ID INT_GIRCA
 AC Q95187;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).
 GN Name=IFNT;


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DR Pfam; PF00143; Interferon, 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Hormone; Pregnancy; Signal.
FT CHAIN 1 23 By similarity.
FT DISULFID 24 195 Interferon tau.
FT DISULFID 52 122 By similarity.
FT DISULFID 162 By similarity.
SQ SEQUENCE 195 AA; 22075 MW; F5304ACB1ACFOCC7 CRC64;

Query Match 72.0%; Score 653; DB 1; Length 195;
Best Local Similarity 75.6%; Pred. No. 1.3e-52;
Matches 130; Conservative 13; Mismatches 29; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKLDNRNRLSPHSCLDRKDFGLPQEMVEGDLQKQAPFVLYEM 60
DB 24 CDLSQNHVLFGRKRLILGQWTRLSPRFCLODRKDFGLPQEMVEGDLQKQAPFVLYEM 83
QY 61 LQGSFNLFTYTHSSAAMDPTTLLEQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPIVTV 120
DB 84 LQGSFNLFTYTHSSAAMDPTTLLEQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPIVTV 143

QY 121 KKYFGIYDYLQEGYSDCAWEIVREMMRALTVSTTLQKRLTKMGDLSNP 172
DB 144 KKYFGIHVYLQEKGYSDCAWEIVREMMRALTVSTTLQKRLTKMGDLSNP 195

RESULT 30
INDL HUMAN STANDARD; PRT; 195 AA.
ID _INDL_HUMAN
AC P37290.
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Interferon delta-1 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94193794; Pubmed=7511610;
RA Whaley A.E., Meka C.S.R., Reddy C.S., Harbison L.A., Hunt J.S.,
RA Imakawa K.;
RT "Identification and cellular localization of unique interferon mRNA
RT from human placenta."
RL J. Biol. Chem. 269:10864-10868(1994).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC -----
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CC -----
DR EMBL; L25664; AAA36123.1; -.
DR PIR; A53746; A53746.
DR HSSP; P56828; 1BSL.
DR GO; GO:0005126; F:hematopoietin/interferon-claas (D200-domain. . .; NMS.
DR GO; GO:0009615; P:response to virus; NAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon, 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Glycoprotein; Multigene family; Signal.
FT SIGNAL 1 23 Potential.

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FT CHAIN 24 195 Interferon delta-1.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
SQ SEQUENCE 195 AA; 21698 MW; BE1CF9E29E29165 CRC64;

Query Match 67.1%; Score 609; DB 1; Length 195;
Best Local Similarity 69.2%; Pred. No. 1.6e-48;
Matches 119; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKLDNRNRLSPHSCLDRKDFGLPQEMVEGDLQKQAPFVLYEM 60
DB 24 CDLSQNHVLFGRKRLILGQWTRLSPRFCLODRKDFGLPQEMVEGDLQKQAPFVLYEM 83
QY 61 LQGSFNLFTYTHSSAAMDPTTLLEQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPIVTV 120
DB 84 LQGSFNLFTYTHSSAAMDPTTLLEQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPIVTV 143

QY 121 KKYFGIYDYLQEGYSDCAWEIVREMMRALTVSTTLQKRLTKMGDLSNP 172
DB 144 KKYFGIHVYLQEKGYSDCAWEIVREMMRALTVSTTLQKRLTKMGDLSNP 195

RESULT 31
Q7M2Y7 PRELIMINARY; PRT; 195 AA.
ID Q7M2Y7
AC Q7M2Y7.
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Interferon alpha-II-10 precursor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92324492; Pubmed=1820971; DOI=10.1016/0303-7207(91)90270-3;
RA Charlier M., Hue D., Boismard M., Martal J., Gaye P.;
RT "Cloning and structural analysis of two distinct families of ovine
RT interferon-alpha genes encoding functional class II and trophoblast
RT (cnp) alpha-interferons."
RL Mol. Cell. Endocrinol. 76:161-171(1991).
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC -----
DR PIR; A61403; A61403.
DR HSSP; P56828; 1BSL.
DR GO; GO:0005126; F:hematopoietin/interferon-claas (D200-domain. . .; IEA.
DR GO; GO:0005126; F:hematopoietin/interferon-claas (D200-domain. . .; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon, 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; FFC53626BF5042B CRC64;

Query Match 67.0%; Score 608; DB 2; Length 195;
Best Local Similarity 69.2%; Pred. No. 2e-48;
Matches 119; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKLDNRNRLSPHSCLDRKDFGLPQEMVEGDLQKQAPFVLYEM 60
DB 24 CDLSQNHVLFGRKRLILGQWTRLSPRFCLODRKDFGLPQEMVEGDLQKQAPFVLYEM 83
QY 61 LQGSFNLFTYTHSSAAMDPTTLLEQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPIVTV 120
DB 84 LQGSFNLFTYTHSSAAMDPTTLLEQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPIVTV 143

QY 121 KKYFGIYDYLQEGYSDCAWEIVREMMRALTVSTTLQKRLTKMGDLSNP 172
DB 144 KKYFGIHVYLQEKGYSDCAWEIVREMMRALTVSTTLQKRLTKMGDLSNP 195

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ID	PRELIMINARY;	PRT;	195 AA.
AC	P28170		
DT	01-NOV-1996 (TREMBlrel. 01, Created)		
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)		
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)		
DE	Interferon omega.		
GN	Name=IFN-omega;		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
EX	MEDLINE=92242937; PubMed=1374107;		
RA	Leeman D.W., Roberts R.M.;		
RT	"Genes for the trophoblast interferons in sheep, goat, and musk ox and		
RT	distribution of related genes among mammals.";		
RL	J. Interferon Res. 12:1-11(1992).		
CC	-1- SIMILARITY: Belongs to the alpha/beta interferon family.		
DR	EMBL, M73245; AAA31507.1; -.		
DR	PIR, I47070; I47070.		
DR	HSSP, P56828; IBSL.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.		
DR	GO; GO:0006952; F:defense response; IEA.		
DR	InterPro; IPRO09079; 4_helix_cytokine.		
DR	InterPro; IPRO00471; Interferon_abd.		
DR	Pfam; PF00143; Interferon; 1.		
DR	PRINTS; PR00266; INTERFERONAB.		
DR	ProDom; PD000550; Interferon_abd; 1.		
DR	SMART; SM00076; IFabd; 1.		
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.		
KW	Antiviral; Cytokine.		
SO	SEQUENCE 195 AA; 21732 MW; 42EF83B80EBE26496 CRC64;		
Query Match	64.7%; Score 587; DB 2; Length 195;		
Best Local Similarity	67.4%; Pred. No. 1.8e-46;		
Matches 116; Conservative	20; Mismatches 36; Indels 0; Gaps 0;		
OY	1 CYLSRKLMLDARENKLLIDRNKRSLSPHSCLDQRKDFGLPQEMVEGDOLQKDDAPFYLYEM 60		
DB	24 CDLSNHNVLVGRKNTLRLLGOMTRLSPHCLQDRKDPARFQEWEEGGLQEQAVLSLHEM 83		
OY	61 LQGSFNLVYVTEHSSAAMPDTLLLEQCTGSLQOGLDHLDTCRGQVGVEEDSEGLNDPIVTV 120		
DB	84 LQGSFNLVHTERRSSAAMNTLLIKQLRNLGLDQLVLDLACLGDGKEEBSALGRTPTLAV 143		
OY	121 KKYFGIYDYLQEKGYSDCAWEIYVENMRALTVSTTLQKRLTXGGLNSP 172		
DB	144 KRYFGIHVYLKEKGYSDCAWEIYVVEIMRSLSSSTLSQERLRIMMDGVNSP 195		
RESULT 33			
ID	Q28561	PRELIMINARY;	PRT; 195 AA.
AC	Q28561;		
DT	01-NOV-1996 (TREMBlrel. 01, Created)		
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)		
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)		
DE	Interferon alpha precursor.		
GN	Name=Amv 124;		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

RX	TISSUE=Embryo;
RC	MEDLINE=93250155; PubMed=8485241;
RA	Nephew K.P., Whaley A.E., Christenson R.K., Imakawa K. ;
RT	"Differential expression of distinct mRNA for ovine trophoblast protein-1 and related sheep type I interferons." ;
RL	Biol. Reprod. 48:768-778(1993) .
CC	-1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR	EMBL; X59067; CAA41790.1; -.
DR	PIR; I46397; I46397.
DR	HSSP; P56828; 1B5L.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005126; F:hematopoietin/interferon-claes (D200-domain. . .); IEA.
DR	GO; GO:0006952; P:defense response; IEA.
DR	InterPro; IPRO09079; 4 helix cytokine.
DR	InterPro; IPRO0471; Interferon_abd.
DR	Pfam; PF00143; Interferon; 1.
DR	PRINTS; PR00266; INTERFERONAB.
DR	PRODom; PD000550; Interferon_abd; 1.
DR	SMART; SM00076; IFabd; 1.
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW	Antiviral; Cytokine; Signal.
FT	SIGNAL
FT	CHAIN
FT	SEQUENCE
SO	195 AA; 21758 MW; 58335195CB7E1448 CRC64;
OY	Query Match
OY	Best Local Similarity 64.5%; Score 585; DB 2; Length 195;
OY	Matches 115; Conservative 20; Mismatches 37; Indels 0; Gaps 0
DB	1 CYLSRKTLMDARENLKILDRMNRSLSPHSCLDPRDKFGLPQEWVEDGLOKDQAFPLVYM 60
DB	24 CDLSQNHVLVSQSNRLTGLQMRRISLRFLCDPRDFAPQEWEVGQIQEAQAIVLHEM 83
OY	61 LQGSFNLFYTHSHSAAMDPTLLLEQLCTGLQQOQLDHLDTFCRGVMGEEDSELGNMPDIVTV 120
DB	84 LQGSFNLFHTHSSAADPTLLLEHVRIGLHQQLDDLDACLGSEVIGEESALGRTEPTLLAM 143
OY	121 KKTYRQGIYDYIOEKGYSDPCAMEIYRVEMRALITVSTTLQKRITTKGGDLNSP 172
DB	144 KTYEGIHVLYIKERKGYSDCAWEIVLEIMRSLSSTSLHKRLRMWDGDLSSP 195
INOT	BOVIN
ID	INOI_BOVIN STANDARD; PRT; 195 AA.
AC	P07352;
DT	01-APR-1988 (Rel. 07, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Interferon omega-1 precursor (Interferon alpha-II-1) (IFN-omega-c1).
GN	Name=IFNW;
OS	Bos taurus (bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovinae; Bos.
RN	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Pancreas;
RX	MEDLINE=85187974; PubMed=2985969;
RA	Capon D.J., Shepard H.M., Goeddel D.V.;
RT	"Two distinct families of human and bovine interferon-alpha genes are coordinately expressed and encode functional polypeptides." ;
RL	Mol. Cell. Biol. 5:768-779(1985).
RN	[2]
RN	SEQUENCE FROM N.A.
RA	Chung Y.G., Seidel G.E. Jr.;
RT	"Cloning bovine interferon-tau genes and characterizing their transcriptional expression during early pregnancy." ;
RL	Submitted (FE8-2000) to the EMBL/GenBank/DBJ databases.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC	-----

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DR EMBL; M11002; AAA30578.1; -.
 DR EMBL; AF238610; AAG14167.1; -.
 DR PIR; B23385; IYBO11.
 DR HSSP; P56828; 1B5L.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon.1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd.1.
 DR PROSITE; PS00252; INTERFERON_A_B_D.1.
 KM Antiviral; Cytokine; Multigene family; Signal.
 FT SIGNAL
 FT CHAIN
 FT DISULFID 24 195 Interferon omega-1.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 SQ SEQUENCE 195 AA; 21980 MW; 1B65FD4BCAB2A15 CRC64;

Query Match 64.2%; Score 582; DB 1; Length 195;
 Best Local Similarity 66.9%; Pred. No. 5.2e-46;
 Matches 115; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

QY 1 CYLSRKMLDAREVLKLLDRNRRLSPHSCLODRKDFGLPQEMVGGDLOKQAPVLYEM 60
 DB 24 CDLSQNHVHVRKQVLVLLHGMRRRLSPFCLODRKDFGLPQEMVGGDLOKQAPVLYEM 83
 QY 61 LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVWGEEDSELGNMDPIVTV 120
 DB 84 LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVWGEEDSELGNMDPIVTV 143
 QY 121 KKYFGIYDVLQEGKGYSDCAMEIVRVMRALVTSTLQKRLTMGGDLNSP 172
 DB 144 KRYFGIYDVLQEGKGYSDCAMEIVRVMRALVTSTLQKRLTMGGDLNSP 195

RESULT 35

Q6SMO8 PRELIMINARY; PRT; 129 AA.
 ID Q6SMO8
 AC Q6SMO8; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Interferon-cauza (Fragment).
 OS Bos mutus grunniens (Yak).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovine; Bos.
 NCBI_TaxId=30521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li Y., Li N., Li S.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL; AY455289; AAR19064.1; -.
 DR HSSP; P56828; 1B5L.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon.1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd.1.
 DR SMART; SM00076; IFabd.1.
 KM Antiviral; Cytokine.1
 FT NON_TER 1

FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14764 MW; DA6E297C8B0AB89 CRC64;

Query Match 58.5%; Score 531; DB 2; Length 129;
 Best Local Similarity 80.2%; Pred. No. 1.7e-41;
 Matches 101; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 8 MLDARENLKLLDRNRRLSPHSCLODRKDFGLPQEMVGGDLOKQAPVLYEM 67
 DB 4 MLDARENLKLLDRNRRLSPHSCLODRKDFGLPQEMVGGDLOKQAPVLYEM 63
 QY 68 FYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVWGEEDSELGNMDPIVTVKRYFGI 127
 DB 64 FYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVWGEEDSELGNMDPIVTVKRYFGI 123
 QY 128 YDYLQE 133
 DB 124 HVTYKE 129

RESULT 36

Q29085 PRELIMINARY; PRT; 190 AA.
 ID Q29085
 AC Q29085; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE PolFN-alpha II-5 protein precursor.
 GN Name=PolFN-alpha II-5;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=domestica; TISSUE=liver;
 RC MEDLINE=92193688; PubMed=1800582;
 RA Lettve F., La Bonnardiere C., Mege D.;
 RT "The porcine family of interferon-omega: cloning, structural analysis
 RT and functional studies of five related genes."
 RL J. Interferon Res. 11:341-350(1991).
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL; X57196; CAA40482.1; -.
 DR PIR; S23711; S23711.
 DR HSSP; P56828; 1B5L.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon.1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd.1.
 DR SMART; SM00076; IFabd.1.
 DR PROSITE; PS00252; INTERFERON_A_B_D.1.
 KM Antiviral; Cytokine; Signal.
 FT SIGNAL
 FT CHAIN
 FT CHAIN 24 190 Interferon-alpha II-5.
 SQ SEQUENCE 190 AA; 21667 MW; D4BAC635AB3E207A CRC64;

Query Match 56.6%; Score 513.5; DB 2; Length 190;
 Best Local Similarity 62.0%; Pred. No. 1.2e-39;
 Matches 106; Conservative 24; Mismatches 36; Indels 5; Gaps 1;

QY 1 CYLSRKMLDAREVLKLLDRNRRLSPHSCLODRKDFGLPQEMVGGDLOKQAPVLYEM 60
 DB 24 CDLSQNHVHVRKQVLVLLHGMRRRLSPFCLODRKDFGLPQEMVGGDLOKQAPVLYEM 83
 QY 61 LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVWGEEDSELGNMDPIVTV 120
 DB 84 LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVWGEEDSELGNMDPIVTV 143
 QY 121 KKYFGIYDVLQEGKGYSDCAMEIVRVMRALVTSTLQKRLTMGGDLNSP 171

RESULT 37	
ID	INQ2 HORSE
ID	INQ2 HORSE
ID	INQ2 HORSE
AC	PO5002; STANDARD; PRT; 195 AA.
DT	13-AUG-1987 (Rel. 05, Created)
DT	13-AUG-1987 (Rel. 05, Last sequence update)
DT	29-MAR-2004 (Rel. 43, Last annotation update)
DE	Interferon omega-2 precursor (interferon alpha-II-2).
DE	Equus caballus (horse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NC	NCBI_TaxID=9796;
RN	[1]
RP	SEQUENCE OF 167-195 FROM N.A.
RX	MEDLINE=87053170; PubMed=3022999;
RA	Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT	"Molecular cloning and expression in Escherichia coli of equine type I
RT	interferons."
RL	DNA 5:345-356(1986).
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: Belongs to the alpha/beta interferon family.
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CC	or send an email to license@isb.ch).
CC	-----
DR	EMBL; M14545; AAA30949.1; -
DR	EMBL; A16557; CAA01283.1; -
DR	PIR; F24912; IVH022.
DR	HSSP; P56828; 1BSL.
DR	InterPro; IPR009079; 4 helix cytokine.
DR	InterPro; IPR00471; Interferon_abd.
DR	Pfam; PF00143; Interferon_1.
DR	PRINTS; PR00266; INTERFERONAB.
DR	ProDom; PD00550; Interferon_abd_1.
DR	PROSITE; PS00522; INTERFERON_A_B_D; 1.
KW	Antiviral; Cytokine; Glycoprotein; Multigene family; Signal.
FT	SIGNAL 1 23
FT	CHAIN 24 195 Interferon omega-2.
FT	DISULFID 24 122 By similarity.
FT	DISULFID 52 162 By similarity.
FT	CARBOHYD 101 101 N-linked (GlcNAc...) (potential).
FT	SEQUENCE 195 AA; 22131 MW; 949DA221AB3C17DF CRC64;
Query Match	55.0%; Score 499; DB 1; Length 195;
Best Local Similarity	57.0%; Pred. No. 2,7e-38;
Matches	98; Conservative 30; Mismatches 44; Indels 0; Gaps 0;
QY	1 CYLSRKLMDARENLKLDNRNRSLSPHSCLQDRKDFGLPQEMVBSGLOKQDAFPVLYEM 60
DB	24 CDLPNHLIVSRKRVLLGQMSRISSAICLKRKDFRFPQPMADGRQPEEAQASVLIHEM 83
QY	61 LQGSNLLVYTESHSAAWDTTLLEQLCTGLQOGLDLDTCRGQVWGEESESLGNMDPIYTV 120
DB	84 LQQLFSLPHTERSAAWMTTLTLDLCTGLRLQLEDLDTCLEDEMGEESALGVAPTLAV 143
QY	121 KRYFGIYDYLQEKGYSDCAMEIVEVMNRALTVSTTLQKRLTRKGGDINSF 172
DB	144 KRYFGIHLVLYLKEKKYSDCAMEIVMEIMRSPSSANLQGRLRMWDGLGSP 195
RESULT 38	
ID	Q29098
AC	Q29098; PRELIMINARY; PRT; 190 AA.

[illegible]

[2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte; PubMed=1647209; DOI=10.1016/0167-4781(91)90004-6;
 RA Adolf G.R., Fruehbeis B., Hauptmann R., Kalener I., Maurer-Fogy I.,
 RA Ostermann E., Patzelt E., Schwendenwein R., Sommergruber W.,
 RA Zsoephel A., Patzelt E., Schwendenwein R., Sommergruber W.,
 RT "Human interferon omega 1: isolation of the gene, expression in
 RT Chinese hamster ovary cells and characterization of the recombinant
 RT protein.";
 RL Blochim. Biophys. Acta 1089:167-174(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Schetz T.E.,
 RA Brownstein W.J., Ueda T.B., Toshiyuki S., Carrincci P., Prange C.,
 RA Raha S.S., Loquiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 22-195 FROM N.A.
 RX MEDLINE=85269605; PubMed=3895159;
 RA Hauptmann R., Sweetly P.,
 RT "A novel class of human type I interferons.";
 RL Nucleic Acids Res. 13:4739-4749(1985).
 RN [5]
 RP SEQUENCE OF 22-36.
 RX PubMed=15340161; DOI=10.1110/pb.04682504;
 RA Zhang Z., Henzel W.J.,
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 RN [6]
 RP SEQUENCE OF N-TERMINUS, AND CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=50264422; PubMed=1693148;
 RA Adolf G.R., Maurer-Fogy I., Kalener I., Cantell K.,
 RT "Purification and characterization of natural human interferon omega
 RT 1. Two alternative cleavage sites for the signal peptidase.";
 RL J. Biol. Chem. 265:9290-9295(1990).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
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 CC -----
 CC EMBL: M11003; AAA52724.1; -;
 CC EMBL: X58822; CAA41626.1; -;
 CC EMBL: BC069095; AA069095.1; -;
 CC EMBL: X02669; CAA26501.1; -;
 CC EMBL: A12140; CAA01011.1; -;
 CC PIR: A93070; IYHUII.
 CC HSP: P01563; IITF.
 CC GlycoSiteDB: P05000; -.

DR Genew; HGNC:5448; IFN1.
 DR MIM; 147553; -;
 DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
 DR GO; GO:0007050; P:cell cycle arrest; TAS.
 DR GO; GO:0009615; P:response to virus; TAS.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR004771; Interferon_abd.
 DR Pfam; PF00143; Interferon_1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR PRODOM; PD000550; Interferon_abd. 1.
 DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
 DR Antiviral; Cytokine; Direct protein sequencing; Glycoprotein;
 KW Multigene family; Signal.
 FT SIGNAL 1 23 Or 21 in some molecules.
 FT CHAIN 24 195 Interferon omega-1.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 FT CARBOHYD 101 101 N-linked (GlcNAc...)
 FT FTid-CAR_000050.
 FT CONFLICT 111 111 G->E (in Ref. 1).
 FT SEQUENCE 195 AA; 22319 MW; 1B4306F34879878A CRC64;
 SQ
 Query Match 52.1%; Score 473; DB 1; Length 195;
 Best Local Similarity 55.6%; Pred. No. 7e-36;
 Matches 95; Conservative 28; Mismatches 48; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKLLDRNRLSPHSCLQDRKDFGLPEWVBDQLQKDAFPVLYEM 60
 DB 24 CDLPQNGLLSRMTLVLLHQRRISPLCLKDRDPFPQGMVGSQLOKXHWVSLHEM 83
 QY 61 LQGSFNLFTYHSSAANDTTLLEOLCTGLQOQDLHDTCKGQVNGEEDSELGNMDDIVTV 120
 DB 84 LQQIFSLFHTERSAANMTLLDQLHTGLHQQLHETCLLQVVGESASACISSPALTL 143
 QY 121 KKYPQGIYDYLOEKGYSDCAWEIVREMMRALFTVSTLQKRLTGMGDLNS 171
 DB 144 RRYQGIKRVLYKRGYSDCAMEVVRMIMKSLFSTMGRLSKRDLS 194
 RESULT 40
 ID 029084 PRELIMINARY; PRT; 179 AA.
 AC 029084;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE PoIFN-alpha II-4 protein precursor.
 GN Name=PoIFN-alpha II-4;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=domestic; TISSUE=liver;
 RX MEDLINE=92193689; PubMed=1800582;
 RA Lettreve F., La Bonnardiere C., Mege D.,
 RT "The porcine family of interferon-omega: cloning, structural analysis
 RT and functional studies of five related genes.";
 RL J. Interferon Res. 11:341-350(1991).
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 CC EMBL: X57195; CAA40481.1; -;
 CC PIR: S23710; S23710.
 CC HSP: P56828; IBSL.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR Pfam; PF00143; Interferon_abd.
 DR PRINTS; PR00266; INTERFERONAB.
 DR PRODOM; PD000550; Interferon_abd. 1.
 DR SMART; SM00076; IFabd; 1.

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DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KM Antiviral; Cytokine; Signal. Potential.
FT CHAIN 1 23
SQ SEQUENCE 179 AA; 20621 MW; 7D55D2ED05ABF0AD CRC64;

Query Match
Best Local Similarity 51.8%; Score 469.5; DB 2; Length 179;
Matches 95; Conservative 26; Mismatches 35; Indels 5; Gaps 1;

QY 1 CYLSRKMLDARENKLLDRNNRLSPHSCLQDRKDFGLPOEMVWGDLQKDAQFPVLYEM 60
DB CDLFQNHVHSRKNLYLRQWRRLSPGCLKDRKDFGPQPMVWGSQLQKTOAIVSLHEM 83

QY 61 LQGSFNLFTYHSSAAMDITLLLEQCTGLQOQLDHLDTCRGQVWGGEEDSELGNMIPVTV 120
DB LQGFLLHFTERSAAMDITLLDLCGLHQHLDLSSCLVQVWGQASALE-----MAV 138

QY 121 KKVFQGIYDYLQEKGYSDCAMEIVRVEMMRALTVSTTLQKR 161
DB 139 KRYFEGIHLYLKEKKYSDCAMEIVRVEMMRALTVSTTLQKR 179

RESULT 41
Q13168 PRELIMINARY; PRT; 174 AA.
ID 013168;
AC 013168;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interferon omega-1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Zeng Q., Li M., Zhou Y., Guo H., Hou Y.;
RC STRAIN=Chinese W1;
RT "The cloning, sequencing of the primary structure and expression in E.
RT coli Chinese human IFN-W1 gene."
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 0:0-0(10).
RN 2;
RP SEQUENCE FROM N.A.
RA Xu L.;
RC STRAIN=Chinese W1;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; U25670; AAA70091.1; -.
DR PIR; PC2204; PC2204.
DR HSSP; P01563; IITP.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KM Antiviral; Cytokine.
FT NON TER 1
SQ SEQUENCE 174 AA; 20249 MW; B1CC9AB593016C5 CRC64;

Query Match
Best Local Similarity 50.9%; Score 462; DB 2; Length 174;
Matches 93; Conservative 26; Mismatches 50; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKLLDRNNRLSPHSCLQDRKDFGLPOEMVWGDLQKDAQFPVLYEM 60
DB 3 CDLPQNHGLSRNTLVLLHQMRRISPLCLKDRRDFRFPQEMVWGSQLQKRAHVMASLHEM 62

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QY 61 LQGSFNLFTYHSSAAMDITLLLEQCTGLQOQLDHLDTCRGQVWGGEEDSELGNMIPVTV 120
DB LQGFLLHFTERSAAMDITLLDLCGLHQHLDLSSCLVQVWGQASALE-----MAV 138

QY 121 KKVFQGIYDYLQEKGYSDCAMEIVRVEMMRALTVSTTLQKR 161
DB 123 KRYFEGIHLYLKEKKYSDCAMEIVRVEMMRALTVSTTLQKR 173

RESULT 42
INOI HORSE
ID INOI HORSE STANDARD; PRT; 195 AA.
AC P05001;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 23-MAR-2004 (Rel. 43, Last annotation update)
DE Interferon omega-1 precursor (Interferon alpha-II-1).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=87053170; PubMed=3022999;
RA Hammler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type I
RT interferons."
RL DNA 5:345-356(1986).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
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CC -----
DR EMBL; M1544; AAA30955.1; -.
DR EMBL; A15991; CA01259.1; -.
DR PIR; E24912; IYHO21.
DR HSSP; P56828; IBSL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KM Antiviral; Cytokine; Glycoprotein; Multigene family; Signal.
FT CHAIN 1 23
FT DISULFID 24 195
FT DISULFID 24 122
FT DISULFID 52 162
FT CARBOHYD 101 101
SQ SEQUENCE 195 AA; 21882 MW; A81C3CFOA7CA9B8E CRC64;

Query Match
Best Local Similarity 49.0%; Score 444; DB 1; Length 195;
Matches 91; Conservative 26; Mismatches 55; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKLLDRNNRLSPHSCLQDRKDFGLPOEMVWGDLQKDAQFPVLYEM 60
DB 24 CDLPASIDLRKQETLVLLHQMRRISPLCLKDRRDFRFPQEMVWGSQLQKRAHVMASLHEM 83

QY 61 LQGSFNLFTYHSSAAMDITLLLEQCTGLQOQLDHLDTCRGQVWGGEEDSELGNMIPVTV 120
DB LQGFLLHFTERSAAMDITLLDLCGLHQHLDLSSCLVQVWGQASALE-----MAV 138

QY 121 KKVFQGIYDYLQEKGYSDCAMEIVRVEMMRALTVSTTLQKR 161
DB 144 KRYFEGIHLYLKEKKYSDCAMEIVRVEMMRALTVSTTLQKR 173

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RESULT 43
ID INAD HUMAN STANDARD; PRT; 189 AA.
AC P01570;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interferon alpha-5 precursor (Interferon alpha-G) (leif G) (Interferon
  alpha-61).
GN Name=IFNA5;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RX MEDLINE=86037205; PubMed=4057246;
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CC protein kinase and an oligoadenylate synthetase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
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CC or send an email to license@ebi.ac.uk).
-----
DR EMBL: V00533; CAA23794.1; -.
DR EMBL: X02959; CAA26705.1; -.
DR EMBL: V00542; CAA23803.1; -.
DR PIR: A92916; IYHU14.
DR HSSP: P01563; 1ITF.
DR GlycoSiteDB: P01570; -.
DR Genew: HGNC:5420; IFNA14.
DR MIM: 147579; -.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); TAS.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR00471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon abd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Direct protein sequencing; Glycoprotein;
KW Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 189 Interferon alpha-14.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
FT CARBOHYD 95 95 N-linked (GlcNAc...).
FT CONFLICT 175 175 L -> F (in Ref. 3).
SQ SEQUENCE 189 AA; 22062 MW; B6B71E2F0D644FE7 CRC64;
Query Match 48.5%; Score 440; DB 1; Length 189;
Best Local Similarity 54.9%; Pred. No. 7.8e-33;
Matches 90; Conservative 26; Mismatches 48; Indels 0; Gaps 0;
QY 1 CYLSRKMLDARENIKLDNRNRLSPHSCLDRKDFGLPQEMVEGDLQKQAFVLYEM 60
DB 24 CNLSQTSILNRRRTILMLAQRRISPFSCLDKRHDFFPEQEPFQNGFOKAQALSVLHEM 83
QY 61 LQGFNLFYTHSSAANDTTLLEQLCTGLQOQDLHLDTCRCQVNGEESLGNMDEIVTV 120
DB 84 MQQFNLFSTKNSSAAMDTELEKRYIELFQQMDLEACVIGEVETPLMDESDILAV 143
QY 121 KKYFGIYDYLQEGYSDCAWEIVREVMRALTVSTLQKRLTK 164
DB 144 KKYQRITLYLMEKYSFCAMEVRAEIRMSLSFSTNLQKRLR 187

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RT genes."
RL Science 212:1159-1162(1981).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=85229953; Pubmed=3891272;
RA Mizoguchi J., Pltha P.M., Raj N.B.K.;
RT "Efficient expression in Escherichia coli of two species of human
RL interferon-alpha and their hybrid molecules."
RL DNA 4:221-232(1985).
RN
RP SEQUENCE OF 14-189 FROM N.A.
RX MEDLINE=85235859; Pubmed=4008999;
RA Lund B., von Gabain A., Edlund T., Ny T., Lundgren E.;
RT "Differential expression of interferon genes in a substrain of Namalwa
RL cells."
RL J. Interferon Res. 5:229-238(1985).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=87024453; Pubmed=3767336;
RA Savelliev V.I., Zlochevsky M.L., Sorokin A.V., Naroditskaya V.A.,
RA Bolotin A.P., Demjanova N.G., Kozlov Y.I., Neznanov N.S.,
RA Gazaryan K.G., Monastyrskaya G.S., Sverdlov E.D.;
RT "[Cloning and the determination of the nucleotide sequences in 2 genes
RL of human leukocyte interferons]."
RL Antibioc. Med. Biotechnol. 31:592-596(1986).
RN
RP SEQUENCE OF 24-58.
RX MEDLINE=98087498; Pubmed=9425112;
RA Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
RT "Identification of nine interferon-alpha subtypes produced by Sendai
RL virus-induced human peripheral blood leucocytes."
RL Biochem. J. 329:295-302(1998).
RN
RP VARIANT ARG-184.
RX MEDLINE=98376207; Pubmed=9712362;
RA Hussain M., Tan T., Ni D., Gill D.S., Liao M.-J.;
RT "A new allele of interferon-alpha17 gene encoding IFN-alpha17b is the
RL major variant in human population."
RL J. Interferon Cytokine Res. 18:469-477(1998).
CC -1- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC activities. Interferon stimulates the production of two enzymes: a
CC protein kinase and an oligoadenylate synthetase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
-----
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-----
DR EMBL: M11026; AAA52725.1; -.
DR EMBL: V00532; CAA23793.1; -.
DR EMBL: M38289; AAA59165.1; -.
DR EMBL: M71246; AAA52713.1; -.
DR PIR: A01835; IYHU9.
DR PIR: A01835; IYHU9.
DR HSSP: P01563; 1ITF.
DR Genew: HGNC:5422; IFNA17.
DR MIM: 147583; -.
DR GO: GO:0005132; F:interferon-alpha/beta receptor binding; TAS.
DR GO: GO:0009615; P:response to virus; TAS.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR00471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon abd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Direct protein sequencing; Multigene family;
KW Polymorphism; Signal.
FT SIGNAL 1 23

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FT CHAIN 24 189 Interferon alpha-17.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
FT VARIANT 184 184 I->R.
FT CONFLICT 57 57 /FTID=VAR 013020.
FT CONFLICT 78 78 H->P (in Ref. 1).
FT SEQUENCE 189 AA; 21728 MM; 0448EABAB9DFC32 CRC64;

Query Match
Best Local Similarity 55.5%; Pred. No. 1.2e-32;
Matches 91; Conservative 25; Mismatches 48; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENLKLDNRNRLSPHSCLODRKDFGLPOEMVEGDQLQKQAPVLYEM 60
Db 24 CDLPQTHSLGNRRRLILLAQGRISPFSCLDKRDHDFGLPOEFPDGNOPKTOAISVLIEM 83

Qy 61 LQGSFNLPTHTSSAAMDPTTLLEQLCTGLQOQDLHLDTCRGQVNGEEDSEIGNMDPIVTY 120
Db 84 IQQTFNLFTSDSSAAMEQSLEKFTSTLYOQLNNLECVIQVGMESTPLMNEDSLIAV 143

Qy 121 KKVFQGIYDYLQEKGYSDCAWEIYRVEMRALTVSTTLQKRLTK 164
Db 144 RKYFORITLYLTEKKYSCAMEIVRAEIMRSLSTSTNLQKILRR 187

RESULT 46
Q28562 PRELIMINARY; PRT; 195 AA.
ID Q28562;
AC Q28562;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ovine Interferon alpha precursor.
GN Name=amy 49;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92039090; Pubmed=1937057; DOI=10.1016/0378-1119(91)90212-T;
RA Whaley A.E., Carroll R.S., Imakawa K.;
RT "Cloning and analysis of a gene encoding ovine interferon alpha-II." ;
RT Gene 106:281-282(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Whaley A.E., Carroll R.S., Imakawa K.;
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL: X59068; CAA4191.1; -.
DR PIR: I46398; I46398.
DR HSP: P01563; IITP.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 195 ovine interferon alpha.
FT SEQUENCE 195 AA; 22006 MM; 388EE700C586A928 CRC64;

Query Match
Best Local Similarity 47.5%; Score 431; DB 2; Length 195;
Matches 54.3%; Pred. No. 5.6e-32;

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Matches 88; Conservative 23; Mismatches 51; Indels 0; Gaps 0;

Qy 11 ARENLKLDNRNRLSPHSCLODRKDFGLPOEMVEGDQLQKQAPVLYEMIQSFNLYT 70
Db 34 SRSLTVLDDQWRVRSPVLCLEKDRDFQPREVNVGSGFQKQVTSVLHEMLQQLFNLLHT 93

Qy 71 EHSSAAMDPTTLLEQLCTGLQOQDLHLDTCRGQVNGEEDSEIGNMDPIVTYKVFQGIYD 130
Db 94 AHSSAAMNNTLLELHAALHQQLGLTCLVQAMGEEDSVLTADSPFLMLKRYFORILY 153

Qy 131 LQEKGYSDCAWEIYRVEMRALTVSTTLQKRLTKMGDLSNP 172
Db 154 LDEKHSGCAMELVRAEIMRSLSTSTNLQKILRR 195

RESULT 47
Q28844 PRELIMINARY; PRT; 195 AA.
ID Q28844;
AC Q28844;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Interferon-omega48.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94132653; Pubmed=8301151;
RA Charlier M., L'Hardon R., Boissard M., Matral J., Gaye P.;
RT "Cloning and structural analysis of four genes encoding interferon-
RT omega in rabbit." ;
RL J. Interferon Res. 13:313-322(1993).
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL: S68999; AAC60525.2; -.
DR HSP: P56828; IBSL.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 195 ovine interferon alpha.
FT SEQUENCE 195 AA; 21981 MM; D4D2E3EF5134A5SF CRC64;

Query Match
Best Local Similarity 47.4%; Score 430; DB 2; Length 195;
Matches 88; Conservative 23; Mismatches 50; Indels 0; Gaps 0;

Qy 11 ARENLKLDNRNRLSPHSCLODRKDFGLPOEMVEGDQLQKQAPVLYEMIQSFNLYT 70
Db 34 SRSLTVLDDQWRVRSPVLCLEKDRDFQPREVNVGSGFQKQVTSVLHEMLQQLFNLLHT 93

Qy 71 EHSSAAMDPTTLLEQLCTGLQOQDLHLDTCRGQVNGEEDSEIGNMDPIVTYKVFQGIYD 130
Db 94 AHSSAAMNNTLLELHAALHQQLGLTCLVQAMGEEDSVLTADSPFLMLKRYFORILY 153

Qy 131 LQEKGYSDCAWEIYRVEMRALTVSTTLQKRLTKMGDLSNP 172
Db 154 LDEKHSGCAMELVRAEIMRSLSTSTNLQKILRR 195

RESULT 48
IN44_HUMAN STANDARD; PRT; 189 AA.
ID IN44_HUMAN;
AC P05014; P13358;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)

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DT 05-JUL-2004 (Rel. 44, last annotation update)
DE Interferon alpha-4 precursor (Interferon alpha-4B) (Interferon alpha-
MI) (Interferon alpha-76).
GN Name=IFNA4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=66037205; PubMed=4057246;
RA Henko K., Brosius J., Fujisawa J.-I., Haynes J.R.,
RA Hochstadt J., Kovacic T., Pasek M., Schambeck A., Schmid J.,
RA Todoroki K., Waelchli M., Nagata S., Weissmann C.;
RT "Structural relationship of human interferon alpha genes and
RT pseudogenes.";
RL J. Mol. Biol. 185:227-260 (1985).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=84307815; PubMed=6089830;
RA Linane A.W., Bellharz M.W., McMullen G.L., Macreadie I.G., Murphy M.,
RA Nieber I.T., Novitski C.E., Woodrow G.C.;
RT "Nucleotide sequence and expression in E. coli of a human interferon-
RT alpha gene selected from a genomic library using synthetic
RT oligonucleotides.";
RL Biochem. Int. 8:725-732 (1984).
RN [3]
RN SEQUENCE OF 24-56.
RX MEDLINE=98087498; PubMed=9425112;
RA Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
RT "Identification of nine interferon-alpha subtypes produced by Sendai
RT virus-induced human peripheral blood leucocytes.";
RL Biochem. J. 329:295-302 (1998).
RN [4]
RN POLYNORPHISM
RX MEDLINE=97474410; PubMed=9335344;
RA Hussain M., Gill D.S., Liao M.-J.;
RT "Both variant forms of interferon-alpha4 gene (IFNA4a and IFNA4b) are
RT present in the human population.";
RL J. Interferon Cytokine Res. 17:559-566 (1997).
CC -1- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC activities. Interferon stimulates the production of two enzymes: a
CC protein kinase and an oligoadenylate synthetase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- POLYNORPHISM: Two forms exist: alpha-4a and alpha-4b (shown here).
CC They seem to be equally abundant.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC -----
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CC -----
DR EMBL; X02955; CAA26701.1; -;
DR EMBL; M27318; AAA52726.1; -;
DR PIR; E23753; IYHU48;
DR PIR; I52347; I52347;
DR HSSP; P01563; IITF.
DR Genew; HGNC:5425; IFNA4.
DR MIM; 147564; -;
DR GO; GO:0005132; P:interferon-alpha/beta receptor binding; TAS.
DR GO; GO:0009615; P:response to virus; TAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR00471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; INTERFERONAB.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine; Direct protein sequencing; Multigene family;
KW Polymorphism; Signal.

FT SIGNAL 1 23
FT CHAIN 24 189 Interferon alpha-4.
FT DISUFID 24 122 By similarity.
FT DISUFID 52 162 By similarity.
FT VARIANT 74 74 T->A (in alpha-4A).
FT VARIANT 137 137 V->E (in alpha-4A).
FT VARIANT 137 137 /FTid=VAR_013002.
FT VARIANT 137 137 /FTid=VAR_013003.
SQ SEQUENCE 189 AA; 21808 MW; 4198P9CC8E2A80C CRC64;
Query Match 47.3%; Score 429; DB 1; Length 189;
Best Local Similarity 54.3%; Pred. No. 8.2e-32;
Matches 89; Conservative 25; Mismatches 50; Indels 0; Gaps 0;
QY 1 CYLSRKMLARENLKLDNRNLSPHSCIDRRDFGLPEQWVGDLQKQAPFVLYEM 60
DB 24 CDLPQTHSLGNRRALITLQAGRIHSFSCDKDRHDFEPEEPDGHOFQKTAISVLEHM 83
QY 61 LQGSFNLPTTHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMEBDSLGNDPIVTV 120
DB 84 IQQTFNLFSTEDSSAAWEGSLLEKFSFTELYQQLNDLEACVIOEGVEETPLMNVDSILAV 143
QY 121 KKTFQGIYDYLOEKXSDCAWEIVRYVDMRALYVSTTLQKRLTK 164
DB 144 RKYFORITLYLTKKXSPCAMEVVRMRSLSPSTWLQKRLRR 187
RESULT 49
ID INNA HUMAN STANDARD; PRT; 189 AA.
AC P01566;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon alpha-10 precursor (Interferon alpha-C) (Ielf C)
DE (Interferon alpha-6L).
GN Name=IFNA10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=81148795; PubMed=6163083;
RA Goeddel D.V., Leung P.W., Dull T.J., Grose M., Lawn R.M.;
RA McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT "The structure of eight distinct cloned human leukocyte interferon
RT cDNAs.";
RL Nature 290:20-26 (1981).
RN [2]
RN SEQUENCE OF 24-53.
RX MEDLINE=98087498; PubMed=9425112;
RA Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
RT "Identification of nine interferon-alpha subtypes produced by Sendai
RT virus-induced human peripheral blood leucocytes.";
RL Biochem. J. 329:295-302 (1998).
CC -1- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC activities. Interferon stimulates the production of two enzymes: a
CC protein kinase and an oligoadenylate synthetase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC -----
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CC -----
DR EMBL; V00551; CAA23812.1; -;
DR PIR; A60937; IYHU48.
DR HSSP; P01563; IITF.

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DR  Genew; HGNC:5418; IFNA10.
DR  MIM; 147577;
DR  GO; GO:0005376; C:extracellular; NAS.
DR  GO; GO:0005132; F:Interferon-alpha/beta receptor binding; ISS.
DR  GO; GO:0009615; P:response to virus; ISS.
DR  InterPro; IPR009079; 4_helix_cytokine.
DR  InterPro; IPR000471; Interferon_abd.
DR  Pfam; PF00143; Interferon; 1.
DR  PRINTS; PR00266; INTERFERONAB.
DR  ProDom; PD000550; Interferon_abd; 1.
DR  PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW  Antiviral; Cytokine; Direct protein sequencing; Multigene family;
KW  Signal.
FT  SIGNAL.
FT  CHAIN 1 23 Interferon alpha-10.
FT  DISULFID 24 189 By similarity.
FT  DISULFID 52 162 By similarity.
SQ  SEQUENCE 189 AA; 21835 MW; CEC680996FDA7068 CRC64;

Query Match 47.3%; Score 429; DB 1; Length 189;
Best Local Similarity 54.3%; Pred. No. 8.2e-32;
Matches 89; Conservative 26; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENLKILDRMNRSLSPHSCLODRKDFGLPOEMVGGDLOKQDAFPVLYEM 60
Db 24 CDLPQTHSLGNRRALLLGQNGRISPSFCLXDRHDFRIPOEFPDGNOPQKAPALSVLHEM 83

Qy 61 LQGSFNLFTYEHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSBLGNMDPIVTV 120
Db 84 IQQTFNLFSTEDSSAAMDEDLDFKCTELVQQLNDLEACVQEVGVETPLMNDSDILAV 143

Qy 121 KKYFGIYDYLOEKGYSDCANEIVREMRALTYSTTLQKRLTK 164
Db 144 RKYFORITLYLERKYSPCAWEVRAEIMRSLSTYNLQKRLR 187

RESULT 50
Q9UMJ3 PRELIMINARY; PRT; 166 AA.
ID Q9UMJ3;
AC Q9UMJ3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IFNA protein (Fragment).
GN Name=IFNA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83299241; PubMed=6310510;
RA Weber H., Weissmann C.;
RT "Formation of genes coding for hybrid proteins by recombination
RT between related, cloned genes in E. coli.";
RL Nucleic Acids Res. 11:5661-5669(1983).
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; M29884; AA52714.1; -.
DR PIR; H42753; H42753.
DR HSSP; P01563; 1ITF.
DR GO; GO:0005376; C:extracellular; IEA.
DR GO; GO:0005132; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFABD; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT NON_TER 1
SQ SEQUENCE 166 AA; 19386 MW; 4152EA2A78361BB8 CRC64;

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Query Match 47.2%; Score 428; DB 2; Length 166;
Best Local Similarity 53.9%; Pred. No. 8.7e-32;
Matches 90; Conservative 24; Mismatches 47; Indels 6; Gaps 2;

Qy 1 CYLSRKMLDARENLKILDRMNRSLSPHSCLODRKDFGLPOEMVGGDLOKQDAFPVLYEM 60
Db 1 CDLPETHSLDNRRTLLMLAQMSRISPSFCLMDRHDFFGPQEEFPDGNOPQKAPALSVLHEM 60

Qy 61 LQGSFNLFTYEHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSBLGNMDPI 117
Db 61 IQQTFNLFSTEDSSAAMDEDLDFKCTELVQQLNDLEACVQEVGVETPLMNDSDI 117

Qy 118 VTKKTYFGIYDYLOEKGYSDCANEIVREMRALTYSTTLQKRLTK 164
Db 118 LAVKKYFRITLYLERKYSPCAWEVRAEIMRSLSTYNLQKRLR 164

Search completed: October 5, 2005, 10:38:16
Job time : 230 secs

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